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285043 H.sapiens I M75.282 Human Ig la M75.39 Human Ig re 285033 H.sapiens I 285297 H.sapiens I 285297 H.sapiens I 28536 H.sapiens I 28503 H.sapiens I 28504 H.sapiens I 28506 H.sapiens I 28506 H.sapiens I 28507 H.sapiens I 28508 H.sapiens I 28517 H.sapiens I 28517 H.sapiens I 28517 H.sapiens I 28517 H.sapiens I 28518 H.sapiens I 28518
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
Ignatovich,O., Tominson,I.M., Jones,P.T. and Winter,G.
XXXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRC Centre for Protein
2QH, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285043.1 GI:1834754
antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            H.Sapiens Ig lambda light chain variable region gene (24-1)ITIIIH34) rearranged; Ig-Light-Lambda; VLambda.
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Submitted (06-FEB-1997) Ignatovich O.,
Engineering, Hills Road, Cambridge CB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSZ85299
HSIGVL033
HUMIGHEPAL
  HSZ85043
HUMIGLDS
HUMIGLVDS
HSZ85033
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HSZ84919
HSZ85036
                                                                                                                                                            HSZ85355
HSZ85038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AR135365
HSZ85171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Biol. In press 2 (bases 1 to 435)
                                                 Ignatovich, 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
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REFERENCE
AUTHORS
TITLE
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HSZ85043
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KEYWORDS
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                                                                                                                                                         ; Search time 2581.68 Seconds (without alignments) 3161.255 Million cell updates/sec
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                                                                                                                                                                                                                                                 US-09-019-441-1
390
1 ATGGCCTGGACTCTGCTCCT......CCCGGTTGACCGTCCTAGGT 390
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Compugen Ltd.
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                            GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                 nucleic search, using sw model
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em_htgo_inv:*
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Maximum DB seq length: 2000000000
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Match Length DB
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No.
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/translation="MAWALLITTLIFOGTGSWAQSALTQPASVSGSPGQSITISCTGT
SSDVGGYNYVSWYQQHPAKAPKLMIYDVSKRPSGVSNRFSGSKSGNTASLTISGLQAE
DEADYYCSSYTSSSTFVFGGGTKLTVLGQPKAAPSVTLFPPSSEEL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473 bp mRNA linear PRI 05-JAN-1995
Human Ig rearranged lambda chain (V-lambda-2.DS) mRNA, V-, J-, and
C-region subgroup II.
                                                                                                                                                                                                                                                                                              /gene="IGL@"
/note="bears the 8.12 idiotype, which is associated with
anti-DNA specificity of SLE autoantibodies; G00-128-432"
384. .417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 AATCGCTTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 473;
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                                                                                                                                                                                             /product-"immunoglobulin lambda-chain"
/protein_id="AAB37029.1"
/db_xref="GI:186135"
/db_xref="GDB:G00-128-432"
                        /chromosome="22"
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/cell_line="EBV-transformed B cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.3%; Score 340.4; DB 9;
92.1%; Pred. No. 2.2e-84;
iive 0; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ų
                                                                                                                                                                                                                                                                                                                                                                                                                                        108
                                                                /cell_type="B lymphocyte"
1. .473
/gene="IGL@"
 DS.
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/isolate="SLE patient
/db_xref="taxon:9606"
                                                                                                                         /gene="IGL@"
/note="G00-128-432"
                                                                                                                                                                                                                                                                                                                                                                         /note="G00-128-432"
418. .>473
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160 c 119 g
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/qene="IGL@"
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Matches 359; Conserv
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HUMIGLVDS
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
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Human Ig lambda L chain subgroup II V-2.DS mRNA, VJ region, partial
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                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
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                                                                                            /tissue_type="peripheral blood"
/cell_type="lymphocyte"
/clone_lib="cDNA library"
/map="22q11.2"
                                                                                                                                                                                                                                                                  Score 340.4; DB 9
Pred. No. 2.2e-84;
0; Mismatches 31
                                                                                                                                                                                                             4
                                                                                                                                                                                                             102
                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 GCGGAGGGACCAAGCTGACCTAGGT 390
                                                                   /rearranged
/clone="24-17ITIIIH34"
                                      /isolate="donor IT"
/db_xref="taxon:9606"
Location/Qualifiers
                                                                                                                                                                                                              ۵
                                                                                                                                                                                                             105
                                                                                                                                                                                             /gene="IGLV"
147 c
                                                                                                                                                                                                                                                                  87.3%;
92.1%;
                                                                                                                                                                  /gene-"IGLV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M75282
M75282.1 GI:186134
                                                                                                                                                                                                                                                                Query Match 87.3
Best Local Similarity 92.1
Matches 359; Conservative
                                                                                                                                                                                .435
                                                                                                                                                    1. .435
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ACCESSION

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Submitted (06-FEB-1997) Ignatovich
Engineering, Hills Road, Cambridge
Location/Qualifiers
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390 GCCGGAGGACCAAGCTGACCGTCCTAGGT 419
                                                                      435 bp
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/clone="24-07ITIIB176"
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/db_xref="taxon:9606"
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Best Local Similarity 91.8%;
Matches 358; Conservative
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Paul, E., Livneh, A., Manheimer-Lory, A.J. and Diamond, B.
Characterization of the human Ig V lambda II gene family and analysis of V lambda II and C lambda polymorphism in systemic lupus erythematosus [published erratum appears in J Immunol 1993 Apr J. Immunol. 147 (8), 2771-2776 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                        C-region; J-region; V-region; immunoglobulin; immunoglobulin lambda; immunoglobulin light chain; variable region subgroup II. Homo sapiens cDNA to mRNA. Homo sapiens
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160 c 119 g 108 t
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384. .417
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Pred. No. 2.2e-84;
                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="22q11.1-q11.2"
/cell type="B lymphocyte"
1. .473
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/note="G00-128-432"
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/gene="IGL@"
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Best Local Similarity 92.1%;
Matches 359; Conservative
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  PRI 06-FEB-1997
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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  435 bp DNA linear F
chain variable region gene
                         .sapiens Ig lambda light chain variable region gene 24-07ITIIB176) rearranged; Ig-Light-Lambda; VLambda
linear
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Pred. No. 6.2e-84;
0; Mismatches 32;
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/clone_lib="cDNA library"
/map="22q11.2"
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PRI 06-FEB-1997
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Sukaryotas, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 435)
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XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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 301 GCTGAGGACGAGGCTGATTATTACTGCAGCTCATATACAAGCAGCAGCACCTCTCGTCTTC 360
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                                                                                                                                    HS285035 19 lambda light chain variable region gene (24-09ITIIC195) rearranged; Ig-Light-Lambda; VLambda.
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Submitted (06-FEB-1997) Ignatovich O., P
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Ignatovich,O., Tomilinson,I.M., Jones,P.T. and Winter,G.
XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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Pred. No. 4.9e-83;
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/cell_type="lymphocyte"
/clone_lib="cDNA library"
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/isolate="donor SW"
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Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G. XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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Matches 355; Conservative 0; Mismatches 35;
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/clone_lib="cDNA library"
/map="22q11.2"
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/db_xref="taxon:9606"
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/clone="25-070IVE158"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone="25-23SWIB16"
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Best Local Similarity 91.0%;
Matches 355; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
Ignatovich,O., Tomlinson,I.M., Jones,P.T. and Winter,G.
XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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                                                                    121 TGCACTGGAACCAGCAGTGAGTTGTATATAACTATGTCTCCTGGTACCAACAACA 180
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Submitted (O6-FEB-1997) Ignatovich O., MRC Centre for Protein
Engineering, Hills Road, Cambridge CB2 2QH, UK
Location/Qualifiers
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antigen receptor; immunoglobulin; immunoglobulin light chain;
immunoglobulin superfamily; rearranged; variable region.
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                                                     301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
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(24-12ITIIIE213) rearranged; Ig-Light-Lambda; VLambda.
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/cell_type="lymphocyte"
/clone_lib="cDNA library"
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0; Mismatches 37
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/organism="Homo sapiens"
/isolate="donor IT"
/db_xref="taxon:9606"
/rearranged
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
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XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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181 CCAGCCAAAGCCCCCAAACTCATGATTTATGAGGTCACTAAGCGGCCCTCAGGGGTCCCT 240
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H.sapiens Ig lambda light chain variable region gene
(25-33SWIIE224) rearranged; Ig-Light-Lambda; VLambda
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Pred. No. 1.1e-81;
0; Mismatches 37;
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/cell_type="lymphocyte"
/clone_lib="cDNA library"
/map="22q11.2"
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Submitted (06-FEB-1997) Ignatovich
Engineering, Hills Road, Cambridge
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/isolate="donor SW"
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/clone="25-33SWIIE224"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
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/cell_type="lamphocyte"
/clone_lib="cDNA library"
/map="22q11.2"
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J. Mol. Biol. In press
2 (bases 1 to 435)
Ignatovich,0.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
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H.sapiens Ig lambda light chain variable region gene
(25-31SWIID182) rearranged; Ig-Light-Lambda; VLambda.
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/cell_type="lymphocyte"
/clone_lib="cDNA library"
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Submitted (06-FBB-1997) Ignatovich O.,
Engineering, Hills Road, Cambridge CB2
Location/Qualifiers
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/isolate="donor SW"
/db_xref="taxon:9606"
/rearranged
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HS285032 435 bp DNA linear PRI 06-FEB-1997 H.sapiens Ig lambda light chain variable region gene (24-05ITIIB54) rearranged; Ig-Light-Lambda; VLambda.
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Ignatovich,O., Tominison,I.M., Jones,P.T. and Winter,G. XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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.larity 90.0%; Pred. No. 8.3e-81;
Conservative 0; Mismatches 39;
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/cell_type="lymphocyte"
/clone_lib="cDNA library"
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/db_xref="taxon:9606"
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2 (bases 1 to 435)
Ignatovich, O.
Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 435)
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XXXThe Creation of Diversity in the Human Immunoglobulin V Lambda
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2QH, UK
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H.Saplens Ig lambda light chain variable region gene
(25-36SWIIF166) rearranged; Ig-Light-Lambda; VLambda.
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Pred. No. 3e-81;
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/cell_type="lymphocyte"
/clone_lib="cDNA library"
/map="22q11.2"
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Submitted (06-FEB-1997) Ignatovich O.,
Engineering, Hills Road, Cambridge CB2
Location/Qualifiers
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/organism="Homo sapiens"
/isolate="donor SW"
/db_xref="taxon:9606"
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RESULT 1 HSZ85364

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Human immunoglobulin light chain variable region mRNA, cell line
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Enkaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Enkaryota, Metazoa, Chordata, Craniata, Vertebrata; Eutheria;
Mammalla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
Boucher,G., Broly,H. and Lemieux,R.
Restricted Use of Cationic Germline VH Gene Segments in Human Rh(D)
Rod Cell Antibodies
Unpublished
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/product=1g light chain variable region"
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/db_xre
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Submitted (21-DEC-1995) Gerard Boucher, Research and Development,
The Canadian Red Cross Society, Transfusion Center of Quebec, 2535
Laurier Boulevard, Ste-Foy, Quebec GIV 4M3, Canada
Location/Qualifiers
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/db_xref="taxon:9606"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	30000	Description	BF975970 602246174	BG756493 602715633	BI820758 603034354	BG685732 602637827	BG759257 602710936	AV693754 AV693754	AV697043 AV697043	BG758901 602713013	BG756342 602713662	BG756874 602710363	BF976229 602245104	BG397302 602439086	AW404692 UI-HF-BL0	AV694861 AV694861	AV699040 AV699040	AV685070 AV685070	BG483745 602503383
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                     153 TGCACTGGAACCAGCAGTGACGTTGTGGTGGTTATAACTATGTCTCCTGGTCCCAACAACAC 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCAGTAATCGCCCCTCAGGGGTTTCT 272
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                                                                                                                                                                                                          Length 880;
                                                                                                                                                                                                          DB 10;
                                                                                                                                                                                                     86.9%; Score 338.8; DB 10;
91.8%; Pred. No. 2.2e-80;
11ve 0; Mismatches 32;
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/db_xref="taxon:9606"
/clone="IMAGE:4855593"
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BG756493
BG756493.1 GI:14067146
                                                                                                                                                                                                     Query Match 86.9
Best Local Similarity 91.8
Matches 358; Conservative
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TITLE
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BG756493
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//issue_type="primary" B-cells from tonsils (cell line)"
//lab_host="DH10B (phage-resistant)"
//lab_host="DH10B (phage-resistant)"
//note="Organ: B-cells; Vector: pOTB7; Site_1: Xho!;
Site_2: BcoR1; cDNA made by oligo-dT priming.
Directionally cloned into EcoR1/Xho! sites using the following 5' adaptor: GGACGAGG(5). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald W. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

7 a 278 c 217 g 161 t
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I (bases 1 to 787)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: Life Technologies, Inc.

CLONA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.6%; Score 334; DB 10;
.larity 91.0%; Pred. No. 4.1e-79;
Conservative 0; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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BI820758
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les 355; Conserv
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/clone="INAGGE: 4765447"
/clone="INAGGE: 4765447"
/clone="INAGGE: 4765447"
/clone="InAGGE: 4766447"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="holl00 (phage-resistant)"
/lab_host="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoR1; CDNA made by oligo-dT priming.
Site_2: EcoR1; CDNA made by oligo-dT priming.
Directionally cloned into EcoR1/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald Mr. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                       Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1624 row: f column: 08
High quality sequence stop: 821.
Location/Qualifiers
I. 829
                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                         Ph.D.
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                         Contact: Robert Strausberg,
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                                                                                                                                                                                                                                     /note="Organ: pooled brain, lung, testis; Vector:
pcMv-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of G male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRv Site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NHLMGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 829)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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602637827F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4765447 5′,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.8%; Score 330.8; DB 1
90.5%; Pred. No. 2.9e-78;
iive 0; Mismatches 37
                         column: 13
                                                                                                            1. 787
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                       /clone="IMAGE:5175684"
/clone_lib="NIH_MGC_115"
/lab_host="DH10B"
                                       High quality sequence start: 2
High quality sequence stop: 785.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLAM11437 row: k
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BG685732
BG685732.1 GI:13917129
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602710936F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851128 5',
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                                                                                                                                                                     61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                  1 ATGGCCTGGACTCTGCTCCTCGTCACCTCTCACTCAGGGCACAGGATCCTGGGCTCAG
                                                                                                         32 ATGGCCTGGGCTCTGCTCCTCCTCACCCTCACGGCACAGGGTCTGGGCCCAG
                                                                                                                                                                                            272 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCGTCTCTGGGCTCCAG
                                                                                                                                                                                                                                                          121 TGCACTGGAACCAGCGATGACGTTGGTGTTATAACTATGTCTCCTGGTACCAACACCAC
                                                                                                                                                                                                                                                                                                                                                                                        212 CCAGGCAAAGCCCCCAAACTCATGATTTATGAGGTCAGTAAGCGGCCCTCAGGGGTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
                                                                                                                                                                                                                                                                                                                                             181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                          ;
0
84.8%; Score 330.8; DB 10; Length 829; 90.5%; Pred. No. 2.9e-78;
                                          Indels
                 Pred. No. 2.9e-78;
0; Mismatches 37
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 716)

S Xu, X., Huang, J., Xu, Z., Olan, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., Hu, G., Gu, J., Chen, Z. and Han, Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Dy comparing Gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

E 1622106

Contact: Zeguang Han Genome Center at Shanghal
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China.
                                                                                     linear EST 16-JAN-2002
05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/dev_stage="Adult"
/lab_host="SOLR"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGCCCCGACTCAGCCTCCCTCTGTGTGTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 ATGCCTGGGCTCTGCTATTCCTCACCCTCCTCACTCAGGGCACAGGGTCCTGGGCCCAG
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AV693754 GKC Homo sapiens cDNA clone GKCGWD05
AV693754
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Pred. No. 7.5e-78;
0; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="GKCGWD05"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="GKC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hanzg@chgc.sh.cn
                                                                                                                                                                    AV693754.1 GI:10295617
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90.38;
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                                                                                                                                                                                                                                                             Homo sapiens
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/lab_host="nbiloB (phage-resistant)"
/note="organ: B-cells; vector: porB?; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGAGGAG(G). Size-selected >500pp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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                                                                                                                           E I (bases 1 to 686)

S NIH-MGC http://mgc.nci.nih.gov/
NIH-MGC http://mgc.nci.nih.gov/
NIH-MGC http://mgc.nci.nih.gov/
NIH-MGC http://mgc.nci.nih.gov/
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
found through the 
                                                                                     Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 7.3e-78;
0; Mismatches 38; Indels 0;
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/db_xref="taxon:9606"
/clone="IMAGE:4851128"
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Best Local Similarity 90.3%;
Matches 352; Conservative (
                                                       Homo sapiens
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="hepatocellular carcinoma"
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/lab_host="SOLR"
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                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 767)
                                                                                                                                                                                                                                                                                                                                                                                               Chinese National Human Genome Center at Shanghai
351 Guo Shouling Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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Pred. No. 7.7e-78;
0; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
198 g
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/clone_lib="GKC"
                                                                                                                                               AV697043.1 GI:10298906
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90.3%;
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/tissue_type="primary" B-cells from tonsils (cell line)"
/lab_host="Drinary" B-cells, vertor: porB?; Site_1: XhoI;
/lab_host="Organ: B-cells, vector: porB?; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >SODDp
for average insert size 1.88b. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Barkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISM Houno sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 786)

RS NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Match Chord Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Contact: Robert Strausberg, Ph.D.

Contact: Innih.gov

Cond Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 786.

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location/Gualifiers

Location/Gualifiers
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301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
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Pred. No. 7.7e-78;
0; Mismatches 38;
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/clone="IMAGE:4853450"
/clone_lib="NIH_MGC_48"
                                                                                                                         BG758901.1 GI:14069554
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Best Local Similarity
Matches 352; Conserv
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/db_xref="taxon:9606"
/clone="Inxes:4853919"
/clone="Inxes:4853919"
/clone="Inxes:4853919"
/clone="Inxes:4853919"
/clone=Lib="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Grgan: B-cells; Vector: pOTB7; Site_1: XhOI;
Site_2: ECGRI; cDNA made by oligo-dT priming.
Directionally cloned into ECORI/XhOI sites using the following 5 adaptor: GGACGAGG(6). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using 2AP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH-MGC Library."
115 a 289 c 222 g 163 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 88)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

AL Unpublished (1999)

AC Contact: Robert Strausberg, Ph.D.

Email: Gapbs-remail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1700 row: 1 column: 16

High quality sequence stop: 810.
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                                                                                                                                                                                                                                                                                                                                           BG756342 889 bp mRNA linear EST 15-MAY-2001 602713662F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853919 5',
 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCCTCAGGGGTCTCT 240
                                                                       241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                                                            GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
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Pred. No. 8.1e-78;
); Mismatches 38; Indels 0;
                                                                                                                                                                                                                 361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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BG756342
BG756342.1 GI:14066995
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90.3%;
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Best Local S1
Matches 352;
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TITLE
JOURNAL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 908)

National Institutes of Health, Mammalian Gene Collection (MGC)

Into Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LCM1692 row: m column: 16

High quality sequence stop: 885.

Location/Qualifiers
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Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkelsy) using ZAP-cDNA synthesis kit (Siratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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/clone_lib="NIH_MCC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
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                                                                                    TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC
                                                                                                                 301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
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/db_xref="taxon:9606"
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BG756874.1 GI:14067527
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G): Size-selected >500bp for average insert size 1.8kb. Library constructed by Li
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/lab_host="DH10B (phage-resistant)"
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
                                                                                                                                                                                                                213 CCAGGCAAAGCCCCCAAACTCATGATTTATGAGGTCAATAAGGGGCCCTCAGGGGTCCCT
                                                             1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCACGGGCACAGGATCCTGGGCTCAG
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 Length 908;
                                38; Indels
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Plate: LLCM1208 row: h column: 02
High quality sequence stop: 777.
Location/Qualifiers
Score 329.2; DB 10;
Pred. No. 8.2e-78;
0; Mismatches 38;
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/db_xref="taxon:9606"
/clone="IMAGE:4336177"
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BF976229.1 GI:12343444
84.48;
90.38;
                                  Conservative
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               Similarity
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                                  352;
Query Match
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JOURNAL
COMMENT
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AUTHORS
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KEYWORDS
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980 bp mRNA linear EST 12-MAR-2001
602439086F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4565516 5',
BG397302
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Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Pittp://image.llnl.gov
Plate: LLCM1282 row: k column: 21
High quality sequence stop: 881.
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Pred. No. 8.4e-78;
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/db_xref="taxon:9606"
/clone="IMAGE:4565516"
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/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library. I others
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Bukaryotas, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 487)
1 Wath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs remail.nih.gov
Enc RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
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Pred. No. 8.4e-78;
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90.3%;
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Ωp ô g ò a ò a ò q ò Q ò g

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/note="Vector: prira-pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (L5-2:Skb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaido, Ph.D. and M. Bento Soares, Ph.D."
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AV694861 GKC Homo sapiens cDNA clone GKCGWE01 5', mRNA sequence.
AV694861.
GKCGWE01 GI:10296724
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1 (bases 1 to 710)

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,O., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma
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found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.0%; Score 327.6; DB 9
.larity 90.0%; Pred. No. 1.7e-77;
Conservative 0; Mismatches 39
                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="inb="NiH_MGC_37"
/clone_lib="NiH_MGC_37"
/csl_Lype="lymph"
/cell_Lipe="germinal center B
/cell_line="MGC85"
/lab_host="DH10B_[LT]"
                        www-bio.llnī.gov/bbrp/image/image.html
Seg primer: M13 Forward.
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Search completed: September 23, 2002, 17:06:45 Job time: 4504 sec
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Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W.,
                                                                                                                                                                                                                                                                                                                   'note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                               Contact: Zeguang Han Genome Center at Shanghai Contact: Zeguang Han Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-50801922 Fax: 86-21-50801922 Fax: 86-21-50801922 This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 TGCACTGGAACCAGCAGTGACGTTGGTAGTTATAACTATGTCTCCTGGTACCAACAACAC 208
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with those of corresponding noncancerous liver
Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
21625106
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                                                                                                                                                                                                                                                                    /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                             84.0%; Score 327.6; DB 9; ilarity 90.0%; Pred. No. 2e-77; Conservative 0; Mismatches 39;
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                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKCGWE01"
/clone_lib="GKC"
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VERSION
KEYWORDS
SOURCE
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                     JOURNAL
MEDLINE
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Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X., M., G., J., Chen, Z. and Han, Z.
Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                    Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801912
Fax: 86-21-50801912
Fax: 86-21-50801912
Fax: 66-21-50801912
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Fax: 66-21-50801912
Fax: 66-21-50801912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 GATGGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ATGCCTGGGCTCTGCTATTCCTCACCTCTCACGGCACAGGGTCCTGGGCCCAG 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="hepatocellular carcinoma"
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 327.6; DB 9;
Pred. No. 2e-77;
0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                      1. .751
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GKGXE07"
/clone=lib="GKC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143
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90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 90.0
Matches 351; Conservative
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DNA encoding novel

Human autoantibody MH4H7 MAb light ch Variable region of Human autoantibody Recombinant human Human ovarian carc

Nucleotide sequenc Nucleotide sequenc Human U266 lambda U266 Lambda gene a Human anti-Pseudom Coding sequence fo Human autoantibody Coding sequence fo Anti-hEDRF antibod

DNA encoding antiDNA encoding antiDNA encoding a var
Monoclonal antibod
DNA encoding novel
EBV transformant a
DNA encoding antiDNA encoding antiHuntingtin intrabo
Huntingtin intrabo
Huntingtin sovel
Nucleotide sequenc
Nucleotide sequenc

Human colon cancer Human foetal liver

Perfect score:

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Run

Sequence:

Scoring table:

Searched:

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Anti-human CD23 6G5 monoclonal antibody light chain variable region DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-human CD23 6G5 monoclonal antibody; light chain variable region; human CD23, 1gE; FeeRii/CD23; gamma 1 constant region; allergy; inflammation; autoimmune disease; allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "anti-human CD23 6G5 light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "CDS does not contain a stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124..165
/*tag= d
/note= "encodes CDR 1 region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                        AAS83478
AAA69957
AAI68755
AAQ36134
                                                                                                                                       AAH42401
AAH42407
AAQ22491
                                                                                                                                                                                                                                   AAH47763
AAS03477
                                                                                                                AAI68765
AAC67868
                                                                                                                                                                                                             AA168759
AA231654
                                                                                                                                                                                                                                                                                                        ABA94221
AAS03509
                                                                                                                                                                                                                                                          AAS03520
                                                                                                                                                                                                                                                                                                                                                                               AAV72228
                                                                                                                                                                                                                                                                                  AAQ55659
                        AAS83483
                                                                                                                                                                                                                                                                                                                                            AAF58707
                                                                                                                                                                                                                                                                                                                                                                                       AAH42391
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1..390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV33307 standard; DNA; 390
 1..57
/*tag= b
58.390
/*tag=_c
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/*tag= e
/*tag=
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                        63.3
63.2
63.2
62.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
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                                                                                                                                                                                                                                                                                                                                         249.2
248.4
246.8
246.6
246.4
244.4
241.8
305.2
303.6
298.8
298.6
297
295.6
                                                                                                                                                               278.4
278.4
275.4
275.4
274.8
271.2
271.2
270.8
269.2
265.8
263.3
                                                                                                                284.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
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  RESULT
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DNA encoding novel
BNA encoding novel
Bicistronic idioty
DNA encoding novel
DNA encoding novel
                                                                              Search time 488.47 Seconds (without alignments) 1370.804 Million cell updates/sec
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Human immune syste
Antibody D lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                 **Sinisting of the control of the co
                                                                                                                                                  1 ATGGCCTGGACTCTGCTCCT......CCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                    3472872
         4.5
Compugen Ltd.
                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                            1736436 seqs, 858457221 residues
                                                                               September 23, 2002, 16:01:56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
            GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG35100
AAS77073
AAS83480
AAS77070
AAF30316
AAS83477
AAS87037
                                                         OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV33307
AAC66528
                                                                                                                                                                          IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                           N_Geneseq_032802:*
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Maximum DB seq length: 200000000
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Database

misc_feature

Score

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321.2 319.6 316.4 313.6 310 307.2 306.8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 390;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 390 BP; 74 A; 123 C; 96 G; 97 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 390; DB 19;
100.0%; Pred. No. 1.6e-109;
iive 0; Mismatches 0;
/note= "encodes CDR 2 region" 328..357
                                                                                                                                                                                                                                                                                                                                                                           Example 1; Pages 102-104; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                  /*tag= f
/note= "encodes CDR 3
                                                                                                                                                                                                                                                  Reff ME;
                                                                                                                                    98WO-US02253
                                                                                                                                                               98US-0803085
                                                                                                                                                                            97us-0803085
                                                                                                                                                                                                                                                  Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                       (IDEC-) IDEC PHARM CORP. (SEGK) SEIKAGAKU CORP.
                                                                                                                                                                                                                                                                                                                                                  auto: immune conditions
                                                                                                                                                                                                                                                                            WPI; 1998-467495/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                         P-PSDB; AAW70377
                                                                                                                                                                                                                                                  Kloetzer WS,
                    misc_feature
                                                                          WO9837099-A1
                                                                                                                                   17-FEB-1998;
                                                                                                                                                                            20-FEB-1997;
                                                                                                                                                               05-FEB-1998;
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                                                                                                      27-AUG-1998
                                                                                                                                                                                                                                                                                                                                    expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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The present invention provides the coding and protein sequences for a number of human immune system associated proteins (HISAPB). These can be used in the diagnosis and treathent of various autoimmune disorders, infections and cell proliferation diseases. The diseases include AIDS, adult respiratory distress syndrome, anaemia, asthma, atherosolearosis, crohn's disease, irritable bowel syndrome, multiple sclerosis, mysthenia gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               d polynucleotides
preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGCCCCGACTCAGCCTCCCTCTGTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 tetgecetgaeteageetgeeteegtgtetgggteteetggaeagtegateaeeatetee 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                 immune system associated protein; HISAP-10; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ATGGCCTGGACTCTGCTCCTCGTCACCTCACTCAGGGCACAGGATCCTGGGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tgcactggaaccagcagtgacgttggtggttataactatgtctcctggtaccaacagtcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                    protein HISAP-10 coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 321.2; DB 22; Length 891;
Pred. No. 2.4e-88;
0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                       Baughn MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              and po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        erythematosus, arteriosclerosis, cirrhosis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human immune system associated proteins (HISAP) a
encoding the HISAP, useful for diagnosing, treating c
immune or cell proliferative disorders or infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 891 BP; 207 A; 287 C; 222 G; 175 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                       Guegler KJ,
                                                                                                                                                               infection; autoimmune disease; cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                       Corley NC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Column 87-90; 54pp; English
                             ΗB
                                                                                                                     associated
                             AAC66528 standard; cDNA; 891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ech 82.4%; al Similarity 89.0%; 347; Conservative
                                                                                                                                                                                                                                                                                  98US-0049672.
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                          (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                     e H, Lal P,
Au-Young J;
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                                                                                                                       system
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Best Local Similarity
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                                                                                                                                                                                              Homo sapiens
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                                                                                      15-FEB-2001
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Lewis AP;
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                   P-PSDB; AAR31025
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 Crowe JS,
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274 aatcggttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccag 333
                  Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;
lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H; ss.
            GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTTC
                                    GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                          Location/Qualifiers
32..739
/*tag= a
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/label= C lambda
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                                                                                                                  Antibody D lambda light chain.
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/label= FR3
359..388
/*tag= h
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/*tag* b

89..154

/*tag* c

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/*tag= e
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243..262
/*tag= f
/label= CDR2
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/*tag= i
/label= FR4
422..736
                                                                             AAQ35100 standard; DNA; 902
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92GB-0006284
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                                                                                                       (first entry)
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853..858
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23-MAR-1992;
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                                                                                                                                                      Synthetic
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The sequences given in AAQ35099-100 encode the heavy and light chains of Antibody D respectively. Antibody D is a monoclonal antibody which was derived from peripheral blood lymphocytes from a hepatitis A virus (HAV) sero positive patient. Antibody D is closely related in nature to murine antibody B5B3. Total RNA was isolated from antibody D expressing cells and polyadenylated RNA was extracted. These polyA RNA's were used to prepare a cDNA library which was screened for human kappa light (L) chains and two positive clones were detected.
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Prodn. of recombinant primate antibodies - useful for treating infections caused by hepatitis A, B and C, herpes, cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.9%; Score 319.6; DB 14; Length 902; 88.7%; Pred. No. 7.6e-88; ive 0; Mismatches 44; Indels 0;
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ID AAS77073 standard; cDNA; 889
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Best Local Similarity 88.7
Matches 346; Conservative
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Best Local Similarity
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                                                                                                                                                      The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerated char reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymerated and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags corrected normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving denotitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in the printed disorders of generated disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Comino acid sequences. AAS64197-AAS34564 represent novel human diagnostic coding sequences of the invention.

Consider the sequence data for this patent did not appear in the printed specification but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 12877; 103pp; English.
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                                                  30-MAR-2001; 2001WO-US08631
                                                                               31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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Best Local Similarity 88.23
Matches 344; Conservative
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P-PSDB; ABG12886.
                                                                                                                                                     Drmanac RT, Liu C,
                                                                                                                           (HYSE-) HYSEQ INC.
WO200175067-A2.
                                                                              31-MAR-2000;
                           11-0CT-2001
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Cand to produce other types of the invention.

Canno acid sequences of the invention.

Canno acid sequences of the invention.

Che sequence data for this patent did not appear in the printed
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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23-AUG-2000; 2000US-0649167
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P-PSDB; ABG19293.
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DB 23; Length 763;

80.4%; Score 313.6; DB 2:89.1%; Pred. No. 4.9e-86;

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14-MAY-2001
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Best Local Si
Matches 340;
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Gaps
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food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                  1 ATGGCCTGGACTCTGCTCCTCGTCACCCTCACTCAGGGCACAGGATCCTGGGCTCAG
                           1 atggcctgggctctgctgctcctcaccctcctcactcaggacacagggtcctgggcccag
                                                       TCTGCCCCGACTCAGCCTCCCTCTGTGTGTGTGTCTCCTGGACAGTCGGTCACCATCTCC
                                                                                            TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTCGTACCAACACCAC
                                                                                                       CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                         GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
                                                                                                                                                                                                         GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAGTAG----CACTTTGTT
 4;
 Indels
                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #12874.
39;
                                                                                                                                                                                                                                             357 ATTCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID No 12874; 103pp; English.
0;
                                                                                                                                                                                                                                                                                                           AAS77070 standard; cDNA; 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000US-0540217.
2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                                                  (first entry)
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-639362/73.
P-PSDB; ABG12883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biodiversity
                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-0CT-2001
Matches 351;
                                                                                                                                                                                                                                                                                                                              AAS77070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1;
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polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to creat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical anging of sites expressing (II). (I) and (II) are useful for treating disorders involving abbrrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AsS64197-AsS4564 represent novel human condition, but was obtained in electronic format directly from WIPO. The type of the protection of commat directly from WIPO. The type of the invention of products of the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 atggcctgggctctgctgctcctcactctcactcaggacacagggtcctgggcccag 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCIGCCCCGACTCAGCCICCCTCTGIGICTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 tgcactggaaccagcagtgatgttggaaattataaccttgtctcctggtaccaacagcac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flt-3 ligand; Fms-like tyrosine kinase; mouse; human; vaccine; immunotherapy; therapy; tumour; lymphoma; gene therapy; VR1642; plasmid VAXID; antibody; idiotype; vector; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 448;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 448 BP; 89 A; 142 C; 113 G; 104 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.5%; Score 310; DB 23;
87.2%; Pred. No. 5.1e-85;
ive . 0; Mismatches .50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 ggacctgggaccaaggtcaccgtcctaggt 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAGAGGACCCGGTTGACCGTCCTAGGT
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Chimeric - Mus musculus.
Chimeric - Homo sapiens.
Chimeric - Bos taurus.
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                        DNA encoding novel human diagnostic protein #19281
                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                        31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                            13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABG19290
                                                                                                                                                                       WO200175067-A2
                                                                                                                                             Homo sapiens,
                                                                                                                                                                                                   11-0CT-2001
                 AAS83477;
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                                                                                                                                                                                                              polynucleotide and one or more antigen, or cytokine encoding polynucleotides, useful for suppressing tumour growth and for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of patient-specific bicistronic chimeric idiotype VR1642 (plasmid VAXID), which is used to treat B-cell lymphoma patients. The plasmid includes the cytomegalovirus immediate-early promoter, enhancer and 5 untranslated sequences, driving the expression of mouse-human chimeric immunoglobulin light and heavy chain sequences. The human light and heavy chain sequences. The human light and heavy chain variable regions are derived from B-cell lymphoma cell line RAMOS. The transcriptional terminator region includes polyA and termination signals from the boxine growth hormone gene. According to the invention, co-administration of VR1642 with a plasmid (see AAF30314) means of treating a patient with B-cell lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 aatcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccag 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCA---CTTTGTTA 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7528 BP; 1896 A; 1980 C; 1847 G; 1805 T; 0 other;
                                                                                                                                                                                                Immunogenic compositions comprising Flt-3 ligand encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.8%; Score 307.2; DB 22; Best Local Similarity 88.3%; Pred. No. 1.1e-83; Matches 346; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                           autoimmune diseases (e.g. rheumatoid arthritis)
                                                                                                                                                                                                                                                                    Example 2; Page 101-106; 149pp; English.
                                                       2000WO-US20679
                                                                                  99US-0146170
                                                                                                                                                                    WPI; 2001-123319/13
                                                                                                               (VICA-) VICAL INC.
WO200109303-A2.
                                                      31-JUL-2000;
                                                                                                                                           Hermanson GG;
                                                                                   30-JUL-1999;
                           08-FEB-2001
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Tang YT;

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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trails to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human DNA and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 78.7%; Score 306.8; DB 23; Best Local Similarity 86.7%; Pred. No. 5.9e-84; Matches 338; Conservative 0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic coding sequences of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
Claim 1; SEQ ID No 19281; 103pp; English.
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AAS83477 standard; cDNA; 756

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WPI; 2001-639362/73
P-PSDB; ABG12884.
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300
                                                                                                                                                                                                                                                                                                                                                                            Human; chromosome mapping, gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                   New isolated polynuclectide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
                                                                                                             241 agtcgcttctctggctccaagtctggcaacacggcctccctgaccatctctgggctccag
                                    CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                      GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
                                                                                                  DNA encoding novel human diagnostic protein #22841.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID No 22841; 103pp; English.
                                                                                                                                                                                      GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                              361 ggcggaggaccagcgtgaccgtccttggt 390
                                                                                                                                                                                                                                                                         AAS87037 standard; cDNA; 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens
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and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                         Score 306.8; DB 23; Length 866;
Pred. No. 6.2e-84;
0; Mismatches 52; Indels 0;
                                                                                                                                                                                                                                                                                                                                       Sequence 866 BP; 200 A; 274 C; 213 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #12875.
                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
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86.7%;
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Best Local Similarity 86.7
Matches 338; Conservative
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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                                                                                                                                                                                                                                                                                                                                    to produce other types of data and products dependent on DNA and no acid sequences. AAS64197-AAS94564 represent novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 305.2; DB 23; Length 453;
Pred. No. 1.5e-83;
0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 453 BP; 83 A; 148 C; 108 G; 114 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                  Claim 1; SEQ ID No 12875; 103pp; English.
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Best Local Similarity 86.4%;
Matches 337; Conservative
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) its useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical fisorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences of data and products dependent on DNA and diagnostic coding sequences of the invention.

Specification but was obtained in electronic format directly from WIPO
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                                                           mapping; gene mapping; gene therapy; forensic;
medical imaging; diagnostic; genetic disorder; ss.
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DNA encoding novel human diagnostic protein #12878.
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llarity 86.2%; Pred. No. 5.3e-83;
Conservative 0; Mismatches 54;
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2000US-0649167
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Matches 336; Conserv
                                                              chromosome
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                                                                                              supplement;
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                                                                                                                                                                    Homo sapiens.
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23-AUG-2000;
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Canding sequences of the invention.

Chock of the printed of portion of mid appear in the printed
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Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
                                           GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
                                                                       gategettetetggetecaagtetgecaacaggeetecetgaecegtetetgggetecag
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                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #19287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 19287; 103pp; English.
                                                                                                                                                       GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                     AAS83483 standard; cDNA; 783 BP
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23-AUG-2000; 2000US-0649167
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P-PSDB; ABG19296.
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                              TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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                                                                                                                Length 783;
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                                                        Sequence 783 BP; 176 A; 253 C; 202 G; 152 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #12873.
                                                                                                                23;
                                                                                                              Score 298.8; DB :
Pred. No. 1.7e-81
); Mismatches 4
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                                                                                                                76.6%;
86.6%;
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                                                                                                                                                       Conservative
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                                                                                                                                  Similarity
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23-AUG-2000;
                                                                                                                Query Match
Best Local Simi
Matches 343;
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                                                          The interior retailed polymorectible (1) and applyapetide (II) sequences (I) be useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymorectides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as imaging of supplement. (II) and its binding partners are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in disorders forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AASG4197-AASG454 represent novel human cald sequence data for this patent did not appear in the printed sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                           Length 414;
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Pred. No. 1.5e-81;
0; Mismatches 39; Indels
                                                     invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                  Sequence 414 BP; 81 A; 140 C; 101 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 novel human diagnostic protein #19289.
                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
                         SEQ ID No 12873; 103pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 76.6%;
Best Local Similarity 89.2%;
Matches 322; Conservative
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags contentifying expressed genes. (I) is useful in gene therapy techniques contentifying expressed genes. (I) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capponities, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human DNA and adagnostic coding sequences of the invention.

Code amino acid sequence data for this partent din ot appear in the printed specification, but was obtained in electronic format directly from WIPO
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Pred. No. 6.2e-81;
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86.5%;
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2000US-0649167
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P-PSDB; ABG19298.
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Best Local Similarity
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                                                                                                                       WO200175067-A2
                                                               sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The colynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or totreat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical inaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biolaiversity and to produce other types of data and products dependent on DNA and canno acid sequences. As564197-AAS94564 represent novel human diagnostic coding sequences of the invention of mutations canno acid sequences of the invention of the printed sequence of the invention of produce data for this patent did not appear in the printed security and product format directly from WIPO conting the printed and product format directly from WIPO conting the printed and product format directly from WIPO conting sequences.
                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss
241 gategettetetggetecatgtetgecaacacggeetecetgacaatetetgggetecag
                                    GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCAC - - - TTTGTTA
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                                                                                                                                                                                                                                                                                                                                                                        DNA encoding novel human diagnostic protein #19282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                     358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID No 19282; 103pp; English.
                                                                                                                                                                                                                                                    AAS83478 standard; cDNA; 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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P-PSDB; ABG19291.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2.
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44 atggcctgggctctgctcatcctcacctcatcagggcacagggtcctgggcccag 103
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                                   Gaps
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                                                                                                                                                                                                                                                                                                                                           241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
                                                                   1 ATGCCTGGACTCTGCTCCTCGTCACCTCCTCAGGGCACAGGATCCTGGGCTCAG
                                                                                                                                    TCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
                                                                                                                                                                                                       TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC
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 Length 876;
                                 49; Indels
 DB 23;
               .7e-80;
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Score 295.6; D
Pred. No. 1.7e-
0; Mismatches
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Best Local Similarity 86.1%;
Matches 341; Conservative
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Search completed: September 23, 2002, 17:58:36 Job time: 7000 sec

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us-09-019-441-1.rnpn

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FEATURE:
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(without alignments)
1896.375 Million cell updates/sec
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76, Appl
267, App
22578, A
28418, A
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13206, A
13540, A
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22578, A
28418, A
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                                                                                                                                                                                                                                                                1 ATGGCCTGGACTCTGCTCCT.......CCCGGTTGACCGTCCTAGGT 390
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/USOG_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USOB_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USOB_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USOB_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USOB_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USOL_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USOL_NEW_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-10-198-846-13206
US-09-918-995-16692
US-09-918-995-16692
US-09-918-995-16692
US-09-918-995-16690
US-09-785-276A-28418
US-10-158-646-73
US-10-158-646-73
US-10-158-646-73
US-10-198-053-267
US-09-918-995-16199
US-09-918-995-16199
US-10-039-785-59
US-10-039-785-63
US-10-139-785-63
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PCT-US02-16106-4
US-10-151-882-4
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                                                                                      nucleic search, using sw model
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Maximum DB
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US-09-919-002-67

US-10-039-785-54

US-10-139-785-54

US-10-139-785-54

US-10-039-785-55

US-10-039-785-57

US-10-039-785-57

US-10-039-785-60

US-10-039-785-60

US-10-039-785-60

US-10-039-785-60

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US-10-039-785-60
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US-10-039-785-55
US-10-139-785-55
US-09-918-995-37811
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ALIGNMENTS

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TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                               NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE:
REPET: P.O. Box 1404
CITY: Alexandria
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-Mar-2002
CLASSIFICATION NUMBER: US/08/803,085
FILING DATE: 25-Mar-2002
REGISTRATION NUMBER: US/08/803,085
FILING DATE: 25-Mar-100:
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
RECISTRATION NUMBER: 35,030
                                                                     APPLICANT: REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
Sequence 1, Application US/10103686 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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1329 AATCGCTTCTCTGGCTCCAAGTCTGGCAACAGGCCTCCCTGACAATCTCTGGGCTCCAG 1270
                                                                                                                                                                                                                                                   62 CTGCCCCGACTCAGCCTCCCTCTGTGTGTGTGTCTGGACAGTCGGTCACCATCTCCT 121
                              CTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCACC
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                                                                                                                                                                  GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
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                                                                                                 181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND METHODS PREVENTION,
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13540, Application US/10198846
GENERAL INFORMATION:
APPLICANT: Lille, James
APPLICANT: Lille, James
APPLICANT: Windyao
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: FOR IDENTIFICATIONS, KITS, AND
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PRE;
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFFWARE: FASTEED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
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90.0%; Pred. No. 4.3e-80;
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US-10-198-846-13540/c
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; ORGANISM: HOMO &
US-10-198-846-13540
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APPLICANT: Lilie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: POR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 60/306,220
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13206
LENTH: 1640
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Pred. No. 2.3e-80;
                                                                                  Length 390;
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                                                                              Score 390; DB 7;
Pred. No. 1.2e-97;
0; Mismatches 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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; Sequence 13206, Application US/10198846
; GENERAL INFORMATION:
                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 390; Conservative 0;
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90.0%;
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Matches 351;
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Gaps 61 1350

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PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FRASLSEQ for Windows Version 3.0
SEQ ID NO 16692
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Best Local Similarity 88.99
Matches 352; Conservative
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Matches 349; Conservative
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                                                                                TYPE: DNA
                                                                                                                                                            Query Match
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: REMM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918, 995
CURRENT APPLICATION NUMBER: US/09/235,076
PRIOR APPLICADION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
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Pred. No. 1.4e-79;
0; Mismatches 41
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36573
LENGTH: 408
                                                                        1169 GCGGAGGGACCAAGCTGACCGTCCTGGGT 1141
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                                               362 GAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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; Sequence 36573, Application US/09918995
; GENERAL INFORMATION:
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Best Local Similarity 89.5
Matches 349; Conservative
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APPLICANT: Wang, YouZhan
APPLICANT: Wang, YouZhan
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
FILLE OF INVENTION: THERAPY OF BREAST CANCER
FILLE REFERENCE: MRI-049
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Length 421;
                                                Indels
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Pred. No. 2.1e-76;
0; Mismatches 38;
  Score 324.4; DB 5
Pred. No. 1.4e-79;
0; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/198,846 CURRENT FILING DATE: 2002-07-18 PRIOR APPLICATION NUMBER: 60/306,220 PRIOR FILING DATE: 2001-07-18
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SOFTWARE: FastSEQ for Windows Version 4.0
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GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC
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Best Local Similarity
                                                                                                RESULT 8
US-09-785-276A-22578
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TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
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                               TCTGCCCCGACTCAGCCTCCCTCTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
                                                                                                                    CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                        GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACC-----AGTAGCACTTTG
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR PILING DATE: 1999-01-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 311.6; DB 5;
Pred. No. 4.6e-76;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 16500
LENGTH: 420
                                                                                                                                                                                                                                                                                                                            Sequence 16500, Application US/09918995 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cch 79.9%; al Similarity 87.4%; 341; Conservative
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Best Local Similarity
Matches 341; Conserv
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US-09-918-995-16500
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GENERAL INFORMATION:
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APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Robert
APPLICANT: Schlegel. Robert
APPLICANT: Schlegel, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSITE CANCER
TITLE OF INVENTION: HUMAN PROSITE
CURRENT APPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-05-25
PRIOR APPLICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-06-25
PRIOR PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-06-25
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR PRIOR FILING DATE: 2000-07-18
PRIOR PRIOR FILING DATE: 2000-07-18
PRIOR PRI
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TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
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                    APPLICANT: Lasek, Amy K.W.
APPLICANT: Sornasse, Thierry
APPLICANT: Sornasse, Thierry
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0030-1 US
CURRENT APPLICATION WUMBER: US/10/158,646
CURRENT FILNG DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/295,239
PRIOR FILING DATE: 2001-05-31
NUMBER OF EEQ ID NOS: 78
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Lasek, Amy K.W.
Springase, Thierry
TILLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0030-1 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 301.8; DB 7;
Pred. No. 2.6e-73;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/158,646
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/295,239
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 76, Application US/10158646 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.48;
87.38;
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                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
    GENERAL INFORMATION:
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LENGTH: 883
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                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF FILE OF INVENTION: HUMAN PROSTATE CANCER CURRENT APPLICATION HUMBER: US/09/785,276A CURRENT FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: 60/183,319 PRIOR FILING DATE: 2000-03-16 PRIOR PAPLICATION NUMBER: 60/189,862 PRIOR APPLICATION NUMBER: 60/189,862 PRIOR APPLICATION NUMBER: 60/207,454 PRIOR APPLICATION NUMBER: 60/207,454 PRIOR APPLICATION NUMBER: 60/211,314 PRIOR PILING DATE: 2000-05-25 PRIOR PILING DATE: 2000-06-09 PRIOR PILING DATE: 2000-06-09 PRIOR PILING DATE: 2000-06-09 PRIOR PILING DATE: 2000-07-18
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Pred. No. 3e-74;
0; Mismatches 36;
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420 tgtcttcggaactgggaccaaggtcaccgtcctaggt 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SEQ ID NO 20418
LENGTH: 1636
                                                                                                      Sequence 28418, Application US/09785276A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-158-646-73 ; Sequence 73, Application US/10158646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 78.3%;
Best Local Similarity 89.2%;
Matches 354; Conservative
                                                                                                                                              APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
                                                                                                                                                                                             APPLICANT: Monahan, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CORGANISM: HOMO Sapiens
US-09-785-276A-28418
                                                            RESULT 9
US-09-785-276A-28418
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Length 883; Indels ဖ

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APPLICANT: Endege, Wilson
APPLICANT: Mondhan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: UNMAN PROSTATE CANCER
FILE REFERENCE: MRI-007B
CURRENT APPLICATION NUMBER: US/09/785,276A
CURRENT FILING DATE: 2001-02-16
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1552 CACTCCTCTTCCTCACCCTCCTCAGGACACAGGGTCCTGGGCCCAGTCTGCCCTGA 1493
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                                                                                                                                                                                                                                                                                                                                                                         GCTGAGGACGAGGCTGATTATTACT-GTTGTTCATATACAACCAGTAGCACTTTGTTATT 359
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                                                                                                                                                                                        GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG
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                                                                                                                                                                  CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.7%; Score 295.2; DB 5; llarity 87.3%; Pred. No. 1.9e-71; Conservative 0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                            360 CGGAAG-AGGGACCCGGTTGACCGTCCTAGG 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR FILING DATE: 2000-07-18
PRIOR APPLICATION NUMBER: 60/255,281
PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Schlegel. Robert
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CORGANISM: Homo sapiens
US-09-785-276A-22578
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Best Local Similarity
Matches 337; Conserv
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US-09-785-276A-22578/c
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                                                                                                                                                                Gaps
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                                                                                                                                                                                                           1 AIGGCCIGGACICICGICGICGICGICGICGICAGGCACAGGAICCIGGGCICAG
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APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.46229
CURRENT APPLICATION NUMBER: US/10/198,053
CURRENT FILING DATE: 2002-07-17
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                     Length 2667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 548;
                                                                                                                                                                Indels
                                                                                                                Score 300.6; DB 7;
Pred. No. 6.8e-73;
0; Mismatches 49;
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0; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cch 75.7%; Score 295.2; al Similarity 87.7%; Pred. No. 1.6s 343; Conservative 0; Mismatches
                       No: 1329881.6
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LOCATION: 346, 358, 432, 510, 512
OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID
US-10-158-646-76
                                                                                                                Query Match 77.1%;
Best Local Similarity 87.2%;
Matches 341; Conservative
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US-10-198-053-267
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Best Local Si
Matches 343;
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311 AGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTA-----TTCGGAA
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; Sequence 16199, Application US/09918995
; GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc.
    TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
    TITLE OF INVENTION: REOM VARIOUS CDNA LIBRARIES
    FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOSS: 38054
; SOOFWARE: FastSEQ for Windows Version 3.0
; TENNAML 413
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ne: 7168 sec
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Best Local Similarity 84.49
Matches 324; Conservative
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Sequence 28418, Application US/09785276A

GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: 1000000
TITLE OF INVENTION: 1000000
TITLE OF INVENTION: 1000000
TITLE OF INVENTION: 1000000
TITLE OF INVENTION: 10000000
FILE REPERENCE: 2000-02-16
FRICH REPLICATION NUMBER: 60/189,862
PRIOR FILING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR PELICATION NUMBER: 60/207,454
PRIOR PELICATION NUMBER: 60/207,454
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-05-16
PRIOR FILING DATE: 2000-06-19
PRIOR PRIOR APPLICATION NUMBER: 60/219,007
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PRIOR FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1636
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Best Local Similarity 87.3%;
Matches 337; Conservative
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US-09-785-276A-28418
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73.8%; Score 288; DB 5;
84.4%; Pred. No. 1.4e-69;
tive 0; Mismatches 60
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TOPOLOGY: 11
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LOCATION:
FEATURE:
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; LOCATION;
US-08-803-085-1
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         161
158.8
1158.8
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; Search time 110.65 Seconds
(without alignments)
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Sequence 133, App
Sequence 132, App
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Sequence 5, Appli
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Sequence 9, Ap
Sequence 25, A
Sequence 8, Ap
Sequence 27, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 43, 7
Sequence 134,
                                                                                                               1 ATGGCCTGGACTCTGCTCCT......CCCCGGTTGACCGTCCTAGGT 390
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Sequence 137,
Sequence 20,
Sequence 3, A
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Sequence 138
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                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-378-939-11
US-08-958-201-13
US-08-958-201-13
US-09-240-274-137
US-09-049-672A-20
US-08-305-683A-3
US-08-305-683A-3
US-09-062-451-241
US-09-062-451-241
US-09-467-550-9
US-08-487-550-9
US-09-049-672A-25
US-09-049-672A-25
US-09-049-672A-25
US-09-049-672A-25
US-09-049-672A-25
US-09-049-04133
US-08-652-816A-27
US-09-240-274-133
US-09-240-274-133
                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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US-09-240-274-134
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US-08-966-316-5
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                                                                                                                                                            383533 seqs, 122816752 residues
                                                             September 23, 2002, 17:07:09
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                                                                                                                                                                                                                                            Listing first 45 summaries
                                           - nucleic search, using sw model
                                                                                                                                  IDENTITY_NUC Gapext 1.0
                                                                                                                                                                                                                                                              Issued_Patents_NA:*
                                                                                                                                                                                                                          Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                               US-09-019-441-1
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273.8
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234.6
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225.8
225.8
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194.8
1194.6
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178.6
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                                                                                                               TCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                   Gaps
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                                                                        1 ATGGCCTGGACTCTGCTCCTCGTCACCTCCTCAGGGCACAGGATCCTGGGCTCAG 60
                                                                                                                                                                                                                                             CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 23, Application US/09049672A

Fatent No. 6135941

GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Au-Young, Janice
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESCONDENCE ADDRESS:
                                   ö
    Length 390;
                                Indels
    Score 390; DB 3; I
Pred. No. 3.3e-106;
                                 ö
                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                     361 GGAAGAGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                          390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304
COMPUTER READABLE FORM:
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APPLICATION NUMBER:
              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
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US-09-049-672A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
Query Match
Best Local 9
                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGGTCTCT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,939
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43;
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0; Mismatches 43
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APPLICANT: CROWE, JAMES SCOTT
APPLICANT: LEWIS, ALAN PETER
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 321.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ERNST & KURZ
N.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82.4%;
                                                                                                                                         LENGTH: 891 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRANY: THYRNOTIO
CLONE: 2872705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 89.00
Matches 347; Conservative
                                                                                                                    SEQUENCE CHARACTERISTICS:
650-845-4166
                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D. C.
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61 TCCTGCACTGGAACCAGCAGTGAGTTGTAAAGTATAAGTCTCCTGGTACCAACAACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 TCCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACAC 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGGTC
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70.6%; Score 275.4; DB 2; Length
Best Local Similarity 89.2%; Pred. No. 2e-72;
Matches 297; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
                                                                 3: Marshall O'Toole Gerstein Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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  materials and methods
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/028,897
FILING DATE: 21-OCT-1996
INFORMATION FOR SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/08958201
Patent No. 5977319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Pope, Anthony R
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific b
                                                                                                                                                                                ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear IMMEDIATE SOURCE:
                                                                                                                                        Illinois
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                                                                                                            Chicago
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                                                                                                                                                        COUNTRY:
                                                                                      STREET:
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Patent No. 5977319
GENERAL INFORMATION:
APPLICANT: Pope, Anthony R
APPLICANT: Pritchard, Kevin
APPLICANT: Williams, Andrew J
APPLICANT: Johnson, Kevin S
TITLE OF INVENTION: Specific binding members for estradiol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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Pred. No. 2.5e-85;
0; Mismatches 44
                                   ATTORNEY AGENT INCORMATION:
NAME: ERNST, BARBARA G
REGISTRATION NUMBER: 30,377
REFERENCE/COCKET NUMBER: 1808-118
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 783-6040
TELEPHONE: (202) 783-6031
INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
LENGTH: 902 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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Best Local Similarity 88.7%;
Matches 346; Conservative
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32..86
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LOCATION:
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70 ACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGA 129
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APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Neil C.
APPLICANT: Gorley, Neil C.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                         Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                      Ouery Match 61.4%; Score 239.6; DB 4; Best Local Similarity 86.8%; Pred. No. 7.4e-62; Matches 276; Conservative 0; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
CURRENT FILING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILING DATE: 1998-04-10
EARLIER APPLICATION NUMBER: 60/028,550
EARLIER FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                  OTHER INFORMATION: anti-Rh(D) chain R01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/09049672A Patent No. 6135941
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        307 accaagctgaccgtccta 324
                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                              LENGTH: 324
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APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE, REFERENCE: 09596-4202
CURRENT APPLICATION NUMBER: US/09/240,274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 CACCCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGTC 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 TCTGATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTC 297
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                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PatentIn Belease #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/958,201
                                                                 E: Marshall O'Toole Gerstein Murray & Bol
6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 273.8; DB 2;
Pred. No. 6e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
  materials and methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 273.8;
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APPLICATION NUMBER: US 60/028,897
RILING DATE: 21-0CT-1996
INFORMATION FOR SEQ 1D NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 137, Application US/09240274 Patent No. 6255455
                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.2%;
                                                                                                                                               COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: D12 (light chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 333 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.9
Matches 296; Conservative
                  NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall (
STREET: 6300 Sears To
    TITLE OF INVENTION:
                                                                                                          Chicago : Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) NAME/KEY: CDS
) LOCATION: 1...3
US-08-958-201-11
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Query Match
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APPLICANT: LAKE, Philip

APPLICANT: NOTTAGE, Barbara

APPLICANT: OSTBERG, Lars G.

TITLE OF INVENTION: WONOCLONAL ANTIBODY TO HERPES SIMPLEX

TITLE OF INVENTION: VIRUS AND CELL LINE PRODUCING THE SAME
NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 935;
                                                                                                                                                                                                                                                                                                                                                                                                                           60.2%; Score 234.6; DB 3; 76.6%; Pred. No. 3.1e-60; tive 0; Mismatches 89;
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                                                                                                                                39,132
                                                                                                            NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                           CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 935 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 60.2
Best Local Similarity 76.6
Matches 301; Conservative
                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
               HEREWITH
                                                                                                                                                                                           TELEFAX: 650-845-4166
APPLICATION NUMBER:
FILING DATE: HEREWI
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CLONE: 2492122
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US-08-305-683A-3
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61 TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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76.3%; Pred. No. 7e-60;
iive 0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "HSV863 light chain
variable region"
                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/305,683A
FILING DATE: 13-SEP-1994
CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/759,279
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 393 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 76.3
Matches 300; Conservative
                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
CCATION: 1..393
OTHER INFORMATION:
US-08-305-683A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                      FILING DATE: 13
CLASSIFICATION:
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                                                                COUNTRY: U
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119 CCTGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACC 178
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Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Snith, John M.
APPLICANT: Snith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER
NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPOTER: IBM PC compatible

COMPOTER: IBM PC compatible

COMPOTER: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/062,451

FILING DATE: 04-APR-1997

CLASSIFICATION:

NAME: Mak1, DAV4d

TLASSIFICATION:

NAME: Mak1, DAV4d

TELECOMMUNICATION INMBER: 210121.419C2

TELECOMMUNICATION INMBER: 210101.419C2
                                                                                                                                                                                                                       3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.9%; Score 225.8; DB 4;
89.0%; Pred. No. 1.1e-57;
tive 0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 TCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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INFORMATION FOR SEQ ID NO: 241:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
EDUTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                       Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                         STREET: 6300 CC
CITY: Seattle
STATE: Washingt
COUNTRY: USA
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                                                                                  APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Stewen G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
CLASSIFICATION: CUNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30; Indels
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Pred. No. 1.1e-57;
0; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: POCTER, Jame E. R.
REGISTRATION NUMBER: 33, 332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ. ID NO: 241:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                      ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CRANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 241:
18-08-991.789A-241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       359 TCGGAAGAGGACCCGGTTGACCGTCCTAGGT 390
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US-08'991-789A-241/c
; Sequence 241, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 771 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.9%;
89.0%;
                                                                                                                                                                                                                                                                                                     STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 89.0 Matches 242; Conservative
                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT .10
US-09-062-451-241/c
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CURRENT APPLICATION DATA
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                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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Matches 285;
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         APPLICANT: Siegel, Donald L.

TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
FILE REFERENCE: 09596-4402
CURRENT APPLICATION NUMBER: US/09/240,274
CURRENT PILLING DATE: 1999-01-29
EARLIER APPLICATION NUMBER: 60/081,380
EARLIER FILLING DATE: 1998-04-10
EARLIER FILLING DATE: 1998-04-10
EARLIER FILLING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCCTGCACTGGA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 -----tgatgttgggaattataaccttgtctcctggtaccaacagtacccaggcaag 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 actcagcctccctccgtgtctgggtctcctggacagtcgatcaccatctcctgcag----
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 312;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ZOLLA-PAZNER, SUSAN
APPLICANT: ZOLLA-PAZNER, SUSAN
APPLICANT: GORNY, MITOSIAV K.
TITLE OF INVENTION: HETEROHYBRIDOMAS PRODUCING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES TO HIV-1
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATE: PSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                            Score 208.8; DB 4;
Pred. No. 9e-53;
0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Browdy and Neimark
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain S01
US-09-240-274-138
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; Sequence 3, Application US/08345321
; Patent No. 5914109
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.5%;
Best Local Similarity 83.6%;
Matches 266; Conservative
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                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 419 Sever CITY: Washington STATE: D.C.
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHRAWACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TCTGTGTTGACGCGCGCCTCAGTGTCTGCGGCCCCAGGACAAAGGTCACCATCTCC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 TGCACTGGAACCAGCGATGACGTTGGTGGTTATAACTATGTCTCCTGGTACCAACACCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TGCTCTGGAAGCAGCTCCAACAT - - TCCCAATAATTATGTATTGTGGTACCAGCAGTTC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 GATCGCTTCTCTGGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGTCCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACC-----AGTAGCACTTTG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 ACTGGGGACGAGGCCGATTATTCTGCGCAACATGGGATAGCGGCCTGAGTGGTGGTTGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 CCAGGCAAAGCCCCCAAACTCATGATTTATGATGTCGCTAAAGCGGGCCTCAGGGGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGCCCTGGACTCTGCTCCTCGTCACCTCCTCAGGGCACAGGATCCTGGGCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.3e-48;
thes 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 GTGTTCGGCGGAGGGACCAAGCTGACGTCCTAAGT 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 194.8; D
Pred. No. 1.3e-
0; Mismatches
                                                                                                                                                                                                                                 ZOLLA-PAZNER1B
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                     FILING DATE:
CLASSIFICATION: 435
PULGATION DATA:
APPLICATION NUMBER: US/07/872,675
US/08/345,321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08487550 Patent No. 6113898 GENERAL INFORMATION:
                                                                                                                                                                             NAME: Browdy, Roger L. REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.9%;
ilarity 72.0%;
Conservative (
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Browdy, Roger L.
                                                                                                                                                                                                                                                                                                                     TELEX: 248633
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHRRACTERISTICS:
LENGTH: 396 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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TCTGCCCCGACTCAGCCTCCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 TGTTCTGGAACCACCTCCAACATCGCAAG -- - TAATTCTGTGCATTGGTACCAATTAGTT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 CCAGGAGCGGCCCCCAAACTCCTCATCTATGCTAATGATCAGCGTGCCTCCGGGGTCCCT 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GATCGCTTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGGTCCAG 300
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                                                                    GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Tang, Y. Tom
APPLICANT: Corley, Nein'
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Banghn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 895;
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Pred. No. 1.9e-48;
0; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OFEKATING SYSTEM: DOS
SOFTWARE: FRAELSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: PF-0497 US TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
       Sequence 25, Application US/09049672A Patent No. 6135941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.9%;
72.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 3174 Porter Drive CITY: Palo Alto STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cerrone, Michael REGISTRATION NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 283; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 650-845-4166
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LUNGTUT13
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; CLONE: 3116314
US-09-049-672A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 GACCGATTCTCTGGCTCCAAGTCTGGTACCGCGGCCTCCCTGGCCATCACTGGGCTCCAG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 TGCACTGGGAGCACCTCCAACATTGGAGGTTAT---GATCTACATTGGTACCAGCACCTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GATCGCTTCTCTGCCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCTGGGCTCCAG 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 AGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGAG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 GCTGAGGACGAGGCTGATTATTACTGTTCATATACAACCAG---TAGCACTTTGTTA
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Pred. No. 1.8e-48;
0; Mismatches 104; Indels 6
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 05/08/487,550

CLASSIFICATION: 435
ATTONREY/AGENT INPOMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030

REFERENCE/POCKET UNBER: 35,030

RECOMMULCATION INFORMATION:
TELECOMMULCATION:
TELECOMMULCATION:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 TrcccAccaccccccccccccccrccTACCT 393
                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 703 836-2021
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.0%;
Matches 283; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: mat_peptide
; LOCATION: 1..711
US-08-487-550-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1..711
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US-09-049-672A-25
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301 GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGT---AGCACTTTGTTA 357
                                                                                          334 CCCGAGGATGAAACTGATTATTACTGTGCAACATGGGATGACAGTGTCAGTGGTTGGATG 393
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Pred. No. 6.7e-48;
0; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
                                                                                                                              358 TTCGGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
                                                                                                                                                      394 TTCGGCGGAGGACCAAGCTGACCTCCTAGGT 426
                                                                                                                                                                                                                                                                                                            APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chutcharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
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ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFRENCE/DOCKET NUMBER: P1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                 Sequence 8, Application US/09079029
Patent No. 6342369
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 49.4%;
Best Local Similarity 74.1%;
Matches 258; Conservative
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LENGTH: 933 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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US-09-079-029-8
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Cercopithecine; Macaca.

1 (bases 1 to 420)
Andris,J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F.,
Blancher, A. and Capra, J.B.
Variable region gene segment utilization in rhesus monkey
hybridomas producing human red blood cell-specific antibodies:
predominance of the VH4 family but not VH4-21 (V4-34)
97368199
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heavy chain variable region, anti-RBC
U57560 Macaca mula U57565 Macaca mula X65910 H.sapiens m U57568 Macaca mula AR062120 Homo sapi X65907 H.sapiens m W57566 Macaca mula X65907 H.sapiens m X65907 H.sapiens m X65908 H.sapiens m AR135375 Sequence AR135375 Sequence AR135375 Sequence 1917843 Sequence 1917844 Sequence 1917844 Sequence 1917843 Sequence 1917843 Sequence 19178743 Sequence 19178775 H.sapiens m AR068233 Sequence
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X65911 H sapiens m
AF62278 Homo sapi
X65909 H sapiens m
AR108863 Sequence
214182 H sapiens r
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Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.
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X65906 H.sapiens m
X67906 H.sapiens r
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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HUMIGHZF
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HSIGHXX23
MMU57566
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HSIGHXX26
HSIGHXX20
AR135375
AR135376
AR026258
HST14X12
HST14X12
HSD44
178743
HSD544
BCO11857
HST14X24
AF062232
AR06813
AR1086813
AR168813
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HSIGHXX25
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AR135359
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Macaca mulatta Ig rearranged
antibody, mRNA, partial cds.
U57560
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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MEDLINE
REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
MMU57560
       ; Search time 2581.68 Seconds (without alignments) 3428.746 Million cell updates/sec
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                                                                                                                                                                                                                      1 ATGAAACACCTGTGGTTCTT......TCCTGGTCACCGTCTCCTCA 423
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                                                                                                                                                                                                                                                                                                                                         3595312
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                        1797656 seqs, 10463268293 residues
                                                                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
                                                                                                                   September 23, 2002, 17:50:03
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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em_htg_inv:*
em_htg_other:*
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length: 2000000000
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/translation="MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSFTLSLTCAVS
GGSFSSYWWGWIRQPPGKGLEWIGSIYGSSGSTEYNPSLKSRATISRDTSKNQFSLKV
SSVTAADTAVYXCARGDXSSNWWYFEFWGQGALVTVSS"
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         Roubinet, F.,
                                                                                                                            2 (bases 1 to 420)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                             Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 7525-9140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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     Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roub Blancher, A. and Capra, J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodipredominance of the VH4 family but not VH4-21 (V4-34) MOI. Immunol. 34 (3), 237-253 (1997)
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/protein_id="AAC02642.1"
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Pred. No. 3.3e-77;
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    /organism="Macaca mulatta"
/db_xref="taxon:9544"
    /note="hybridoma 1C9"

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Macaca mulatta Ig rearranged heavy
antibody, mRNA, partial cds.
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Matches 365; Conservative
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         AUTHORS
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/product="immunoglobulin heavy chain"
/product=1d="AAC02637.1"
/db_xref="d1:1575068"
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SYSISSGYGWNWIRQPPGKGLEWIGSGRGSRGNTNHNPSLKSRVTISIDTSKNQFSLK
GRSISSGYGWNATRQPPGGYSSRFPDYWGQGVLVTVSS"
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Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
and Capra,J.D.

Direct Submission
Submissed (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Taxas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
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Macaca mulatta Statesoa; Chordata; Craniata; Vertebrata; Eutelee
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelee
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
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                                                                                                                                                                                                                                                                                                                                                                                     Score 323.8; DB 9;
Pred. No. 1.6e-78;
0; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                          /organism="Macaca mulatta"
                                                                                                                                           /db_xref="taxon:9544"
/note="hybridoma 1C8"
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87.0%;
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Best Local S:
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Best Local Similarity 87.1
Matches 371; Conservative
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GGSISSNYWSWIRDPGKGLEWIGRRYGTSGSTYYNPSLTSRVTISTDTSKNQFSLKL
SSVTAADTAVYYCARXTVSKABDYWGGGVLVTVSS"
124 c 115 g 91 t
                                                                                               Cercopithecinae; Macaca.

1 (bases 1 to 411)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A. and Capra, J.D.
Variable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
MO1. Immunol. 34 (3), 237-253 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                             2 (bases 1 to 411)
Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Blancher,A.
and Capra,J.D.
Direct Submission
                                                                                                                                                                                                                                                                                                       Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA Location/Qualifiers
                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9; Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="immunoglobulin heavy chain"
/protein_id="AAC02640.1"
/db_xref="GI:1575074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.2%; Score 318.2; DB 9
llarity 88.2%; Pred. No. 5.4e-77;
Conservative 0; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Macaca mulatta"
/db_xref="taxon:9544"
/note="hybridoma 1B4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
U57563
U57563.1 GI:1575073
                                              rhesus monkey.
                                                              Macaca mulatta
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Matches 373; Conserv
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PRI 26-JUL-1997
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
                                                                                                                           heavy chain; immunoglobulin; joining region;
                                                                                                                                                                                                                                                                                          Schiff,C.

Direct Submission

Submission

Submission

Submission

Submission

Submission

Submission

Submission

Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE

2 (bases 1 to 423)

Millil,M., Le Deist,F., de Saint-Basile,G., Fischer,A.,

Fougereau,M. and Schiff, Submission

Bone marrow cells in X-linked agammaglobulinemia express

pre-B-specific genes (lambda-like and V pre-B) and present

immunoglobulin V-D-J gene usage strongly biased to a fetal-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CTGCAGCTGCAGGAGTCGGGCCCAAGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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H.sapiens mRNA for XLA IG heavy chain VDJ region (LE 4-8) X65910.1 GI:39510R
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87.1%; Pred. No. 2.8e-76;
Live 0; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Clin. Invest. 91 (4), 1616-1629 (1993) 93232287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="bone marrow"
/cell_type="pre-B"
/clone_lib="LE library"
/clone="LE 4-8"
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/db_xref="taxon:9606"
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/note="joining region"
120 c 123 g
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                                                                                               X65910.1 GI:395108
diversity region; Ig
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TGCGCTGTCTCTGGTTACTC - - - CATCAGCAGTAACTACTGGAGCTGGATCCGCCAGCCC 177
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462 c 385 g
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Best Local Similarity 84.5%;
Matches 370; Conservative
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Best Local Similarity
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Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC
antibody, mRNA, partial cds.
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SYSISSNYWSWTRQPPCKGLEWIGITYGSSGSAYYNPSLKSRVTISIDTSKNQFSLKL
SSYTAADTAVYYCPYFDYKGPYFDYWGQGVLVTVSS"
128 c 110 g 93 t
                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Macaca.

1 (bases 1 to 114)

Andris,J.S., Miller,A.B., Abraham,S.R., Cunningham,S., Roubinet,F., Blancher,A. and Capra,J.D.
Variable region gene segment utilization in rhesus monkey
bypridomas producing human red blood cell-specific antibodies:
predominance of the VH4 family but not VH4-21 (V4-34)

Mol. Immunol. 34 (3), 237-253 (1997)

2 (bases 1 to 414)
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Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                        298 CTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGATTCG
                                                                                     358 GGATTTTTGGAGTGGTTATCCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCCTC
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/protein_id="AAC02645.1"
/db_xref="GI:1575084"
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Pred. No. 5.3e-76;
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/db_xref="taxon:9544"
/note="hybridoma"
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Best Local Similarity 87.5%;
Matches 370; Conservative
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U57568.1 GI:1575083
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1 (bases 1 to 1431)
Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.
Human B7.1-specific primatized antibodies and transfectomas
expressing said antibodies
Patent: US 6113898-A 11 05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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              CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG
CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC
                                                                    AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
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Pred. No. 1.3e-75;
0; Mismatches 53
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420 bp mRNA linear PRI 26-JUL-1997
X65907 S58702
X65907.1 GI:395105
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(bases 1 to 420)

Schiff,C.

Direct Submission

L. Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE

E. 2 (bases 1 to 420)

S. Milli,M., Le Deist,F., de Saint-Basile,G., Fischer,A., Fougereau,M. and Schiff,C.

Fougereau,M. and Schiff,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X65907.1 GI:395105 diversity region; Ig heavy chain; immunoglobulin; joining region;
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                                                                                        CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                                                                                                                                         TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
                    AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                                      361 GCCCAAATAGCTGGAACAACG----CTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC
                                                                     CCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACTAC
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J. Clin. Invest. 91 (4), 1616-1629 (1993)
93232287
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/cell_type="pre-B"
/clone_lib="LE library"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/note="joining region"
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Homos Sapiens clone 21u-39 immunoglobulin heavy chain variable
AF062120
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GGSISSSNWWSWVRQPPGKGLEWIGEIYHSGSTNYNPSLKSRVTISVDKSKNQFSLKL
SSVTAADTAVYYCARGPPDYGDYRYFDYWGQGTLVTVSSG"
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7
                                                                                                                                                                                                                                                                                                                    Homo saplens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
Wang,X. and Stollar,B.D.
Wang,X. and Stollar,B.D.
Clin. Immunol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-APR-1998) Biochemistry Department, Tufts University School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="immunoglobulin heavy chain variable region"
/protein_id="AAC18156.1"
/db_xref="GI:3170703"
 405
                                 420
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 ---CGCTAGGCTTCTGGGGCCAGGGAGTC
                    361 CTTTTTCAGTTGTTGGAATGGTTTACAACAACTGGTTCGATGTCTGGGGCCCGGGAGTC
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/tissue_type="blood"
/note="from elderly repertoire 21u"
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86.6%; Pred. No. 2.1e-75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
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Wang, X. and Stollar, B.D.
Direct Submission
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/clone="21u-39"
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58. .>426
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361 GCCCAAATAGCTGGAACAA-
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Length 420; Score 311; DB 9; Pred. No. 5.2e-75; 73.5%; 85.1%; Query Match Best Local Similarity

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Human immunoglobulin heavy chain variable region (VH IV family) from IgM rheumatoid factor.
L29122
L29122.1 GI:465144
Ig heavy chain; rheumatoid factor; variable region subgroup VH-IV. Homo saplens CDNA to mRNA.
                 /translation="mkHLMFFLLLVAAPRWVLSQLQLQESGPCLVKPSFTLSLTCTVS
GGSISSSFYWGWIRQPPGKGLEWIGSIYYSGSTYYNPSLKSRVTISVDTSKNQFSLKL
SSVTAADTAVYYCARRSPRIVGANKDVWGQGTTVTVSS"
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 468)
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llarity 85.1%; Pred. No. 9.8e-75;
Conservative 0; Mismatches 60
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     /db_xref="GDB:G00-128-528"
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/note="G00-128-528"
126 c 121 g
                                                                                                                                                                                                                        /standard_name="CDR-2"
/note="G00-128-528"
                                                                                                                                                       /standard_name="CDR-1"
/note="G00-128-528"
                                                                    58. .420
/gene="IGHV@"
/note="G00-128-528"
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/gene="IGHV@"
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/gene="IGHV@"
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/gene="IGHV@"
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Weng, N.P., Yu-Lee, L.Y., Sanz, I., Patten, B.M. and Marcus, D.M.
Structure and specificities of anti-ganglioside autoantibodies associated with motor neuropathies
J. Immunol. 149 (7), 2518-2529 (1992)
                                                                                                                     121 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
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Human (clone R5A3H) Ig rearranged H-chain mRNA V-region,
M99607
   3;
   Indels
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/protein_id-"AAA52982.1"
/db_xref-"G1:185496"
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 90;
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Homo sapiens female adult blood cDNA
 Mismatches
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/tissue_type="blood"
/dev_stage="adult"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14q32.33"
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/gene="IGHV@"
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H.Sabiens mRNA for Ig heavy chain variable region (VH4DJ) (clone
275399
                                                                                                                                                                                                                                                                                              /translation="MKHLWFFLLLVAAPRWVLSQVQLQESGPGLVKPSGTLSLTCAVS
GGSISSSNWWSWYRQPPGKGLEWIGEIYHSGSTNYNPSLKSRYTISVDKSKNQFSLKL
SSVTAADTAVYZCARGHSSWAFDYWGQGTLVTVSSGSASAP"
1 138 c 139 g t 98 t
                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                Human rheumatoid factors with restrictive specificity for rabbit immunoglobulin G: auto- and multi-reactivity, diverse VH gene segment usage and preferential usage of V lambda IIIb J. Exp. Med. 179, 1445-1456 (1994)
             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AACCCGTCCACAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGAACCTGAACTCTGTGACCGCGGGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 GGGCATAGCAGCAGCTGGCTTTGACTACTGGGCCAGGGAACCCTGGTCACCTCTCC 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCTCAG 97
Fang,Q., Kannapell,C.C., Gaskin,F., Solomon,A., Koopman,W.J.
Fu,S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="immunoglobulin heavy chain VDJ region"
/protein_id="AAAA20138.1"
/db_xref="GI:465145"
                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                    Score 309.8; DB 9;
Pred. No. 1.1e-74;
0; Mismatches 47;
                                                                                                                                                                                     /tissue_type="peripheral blood"
                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9666"
/map="14432.3"
/cell_line="KES 643"
/cell_type="non-T"
                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                    73.2%;
86.8%;
                                                                                                                                                                                                         /gene="IGH@"
<38. .>468
                                                                                                                                                                                                                        <38. .>468
/gene="IGH@"
                                                                                                                                                                                                                                                                                                                                                                                                           367; Conservative
                                                                                                          .468
                                                                                                                                                                                               .468
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                    93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCA 423
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Best Local
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MEDLINE
FEATURES
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          AUTHORS
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                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGGAAGGGACTGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGCCCACCAACTAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ATGAAACACCTGTGGTTCTTCTTCCTCCTGGTGGCACTCCCAGATGGGTCCTGTCTTCAG 60
                                                                                                                                                         Boubli, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="Ig heavy chain variable region (VH4DJ)" 57. .351
/note="Ig VH4-segment" 3352. .375
                      chain; immunoglobulin
                                                                                                Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٠<u>.</u>
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                                                                                                                             1 (bases 1 to 414)
Tonnelle,C., D'Ercole,C., Depraetere,V., Metras,D.,
Fougereau,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 305.6; DB 9;
Pred. No. 1.6e-73;
0; Mismatches 49;
275399.1 GI:2062062
immunoglobulin; immunoglobulin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="T22.26"
/dev_stage="infant"
/tissue_type="thymus"
/cell_type="B-!hymhocyte"
/clone_lib="T22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86

    414
    /organism="Homo sapiens"

                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606'
/chromosome="14"
                                      superfamily; variable region.
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86.3%;
                                                                                                                                                                                                                                                                      2 (bases 1 to 414)
Tonnelle, C.
Direct Submission
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Cercopithecinae; Macaca.

1 (bases 1 to 435)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Roubinet, F., Blancher, A. and Capra, J.D.
Blancher, A. and Capra, J.D.
Wariable region gene segment utilization in rhesus monkey hybridomas producing human red blood cell-specific antibodies: predominance of the VH4 family but not VH4-21 (V4-34)
MOL Immunol. 34 (3), 237-253 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MKHLWFFLPLVAAPRWVLSQVQLOKSGPGLVKLRKTLSLTCAVS
GGSVRSNSWWSWIRQPPGKGLEWIGYISGSDGWTFYDPSLKSRVTISTDTSKNGFSLK
LISVTAADTAVYXCARGGFRDDGYTFYRPGDSWGQGVLITVSS"
1 127 c 124 9 8 t
                                                                                                                                                                                                                                                                                                                  PRI 11-FEB-1998
                                                                                                                                                                                                                                                                                             Macaca mulatta Ig rearranged heavy chain variable region, anti-RBC antibody, mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 435)
Andris, J.S., Miller, A.B., Abraham, S.R., Cunningham, S., Blancher, A.
and Capra, J.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center,
University of Texas Southwestern Medical Center, 6000 Harry Hines
Blvd., Dallas, TX 75235-9140, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                    rhesus monkey.
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                  CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCCAGAGATTGG 360
                                                                                                                    G-----GTACCCCCAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCTCC 411
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                                                                                               361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="immunoglobulin heavy chain"
/protein_id="AAC02643.1"
/db_xref="G1:1575080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 303.4; DB 9;
Pred. No. 6.4e-73;
0; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Macaca mulatta"
/db_xref="taxon:9544"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="hybridoma 1E8"
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                                                                                                                                                                                                                                                                                                                                                                                               U57566.1 GI:1575079
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VERSION
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MEDLINE
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AUTHORS
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JOURNAL
                                                                                                                                     358
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                  301
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                                                                                                 HSIGHXX23
H.Saplens mRNA for XLA IG heavy chain VDJ region (LE 4-30).
X65905. S59754
A65905.1 GI:395103
diversity region; Ig heavy chain; immunoglobulin; joining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;;
5
                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-APR-1992) C. Schiff, Centre D'Immunologie de Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE
2 (bases 1 to 414)
Milili,M., Le Deist,F., de Saint-Basile,G., Fischer,A., Fougereau,M. and Schiff,C.
Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTGCAGCTGCAGGAGTCGGCCCCAGGAGTGCTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACCCGTCCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
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                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalla; Eutheria; Primates; Catarrhinl; Hominidae; Homo.
1 (Seses 1 to 414)
Schiff,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6
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93232287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.1%; Score 305; DB 9;
86.1%; Pred. No. 2.3e-73;
tive 0; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="bone marrow"
/cell_type="pre-B"
/clone_lib="LE library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354. .365.
/note="diversity region"
366. .414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366. .414
/note="joining region"
125 c 122 g
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                                                                                                                                                                                                                                                                                                                                    PRI 08-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 423)
Wang, X. and Stollar, B.D.
Direct Submission
Submitted (02-406-1999) Biochemistry Department, Tufts University
School of Medicine, 136 Harrison Ave., Boston, MA 02111, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 423)
                                                                                                                                                                                                                                                                                                                          Homo sapiens clone 77u-c29 immunoglobulin heavy chain variable region precursor (IgH) mRNA, partial cds.
AF174036
AF174036.1 GI:5834031
                                                                           361 GCCCAAATAGCTGGAACAACGCT-----AGGCTTCTGGGGCCAGGGAGTCCTG 408
                                                                                                                                                                                                  /gene="IgH"
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58, 423
TGCGCTGTCTCTGGTGGCTCTGTCAGGAGTAATAGTTGGTGGAGCTGGATCCGCCAGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'product="immunoglobulin heavy chain variable region
                          181 CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCCACCAACTAC
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1. .>423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang,X. and Stollar,B.D. Immunoglobulin VH gene expression in human aging Clin. Immunol. 93 (2), 132-142 (1999) 99459182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heavy chain; immunoglobulin; joining region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like
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Submitted (08-ARR-1992) C. Schiff, Centre D'Immunologie
Marseille, Case 906, 13288 Marseille, Cedes 9, FRANCE
2 (bases 1 to 432)
Millil, M., Le Delst, F., de Saint-Basile, G., Fischer, A.,
Fougereau, M. and Schiff, C.
                                                                                                                                                                             6
                                                                                                                            Length 423;
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                                                                                                                            Score 302.8; DB 9;
Pred. No. 9.3e-73;
0; Mismatches 47;
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/gene="IgH"
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Mammalia; Eutheria;
1 (bases 1 to 432)
Schiff, C.
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                                                                                                                                                                    Query Match 71.3%; Score 301.8; DB 9; Length 432; Best Local Similarity 84.6%; Pred. No. 1.8e-72; Matches 368; Conservative 0; Mismatches 52; Indels 15;
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1. .57
58. .352
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1 ATGAAACACCTGTGGTTCTT.....TCCTGGTCACCGTCTCCTCA 423
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                                               OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery

No. Score Match Length DB ID

1 301.6 71.3 453 9 AW402337
2 301.4 71.3 862 10 BG397580 BG685428 G02637281
3 299 70.7 867 10 BG68428 BG685428 G02637281
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5 288.4 68.2 850 10 BG686474 BG686444 G02637417
7 288.2 68.1 939 9 AL55.672 BG68644 G02637417
8 285.4 67.5 820 10 BG770055 BG68644 G02637417
10 283.2 67.0 814 10 BG68335 BG68529 G02637564
11 280.6 66.3 64.3 10 BG685325 BG685592 G02637564
12 280.6 66.3 64.3 9 AU34293 BG685592 G02637569
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17 279.6 66.1 894 10 BG548421 BG77016 G02714787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
NA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be found through the I.M.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLCM1281 row: g column: 05
High quality sequence stop: 827.
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11H-MGC http://mgc.nci.nih.gov/. National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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M. Staudt, Ph.D. Library preparation
Bonaldo, Ph.D. and M. Bento Soares,
1 145 c 129 g 1 t
                                                                                                                                                 49,
                                                                                                              DB 9;
                                                                                                            Score 301.6; DB 9
Pred. No. 6.9e-68;
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                                                                                                                                                 0; Mismatches
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BG397580
BG397580.1 GI:13291028
                                                                                                            71.3%;
86.9%;
                                                                                                                                                 Matches 344; Conservative
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                                    BASE COUNT
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/note__Organ: B-cells; vector: porB7; Site_1: XhoI; /note__Organ: B-cells; vector: porB7; Site_1: XhoI; Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into ECORIXAhOI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp Hong in the laboratory of Gerald M. Rubin (University of california, Berkeley) using ZAP-CDNA synthesis kit (Strategene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 867)
NTH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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                                                                                                                                                                                                                                                                Length 862;
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/lab_host="DH10B (phage-resistant)"
                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                71.3%; Score 301.4; DB 10;
85.3%; Pred. No. 1e-67;
ive 0; Mismatches 56;
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BG685428.1 GI:13916825
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Matches 361; Conservative
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                                                                                                                                                             /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)" /note="Gran: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                                                                                                                                                                                                                                                                                                                                                                                                 70.7%; Score 299; DB 10; Length 867; ilarity 84.9%; Pred. No. 4.4e-67; Conservative 0; Mismatches 60; Indels
                                           Plate: LLCM1623 row: a column: 21
High quality sequence stop: 637.
Location/Qualifiers
                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                     /clone="IMAGE:4764956"
/clone_lib="NIH_MGC_48"
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Matches 359; Conserv
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Anote—"Organ: pooled lung and spleen; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA source anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dr primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kD, insert size range 1-3 kD, inbrary is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note: this is a NIHMGC Library."
Euteleostomi;
                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1522 row: f column: 06
High quality sequence stop: 794.

Location/Qualifiers
1. 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                   NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 798)
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Pred. No. 8e-65;
0; Mismatches 63; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5208197"
/clone=lib="NIH-MGC_122"
                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B"
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Best Local Similarity 83.7%;
Matches 354; Conservative (
                                                                                                                                                      Unpublished (1999)
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/ Organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/lab_host="DHIDB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: Xhol;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: gGCACGAGG(). Size-selected >SODOp for average insert size 1 8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E I (bases 1 to 850)

E I (bases 1 to 850)

L Unpublished (1999)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Plate: LLCA1623 row: b column: 06

High quality sequence stop: 759.

Location/Qualifiers
                                                                                                                                                                                                       BG686474 11-MGC_48 Homo sapiens cDNA clone IMAGE:4764965 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/tissue_type="placenta"
/note="vector: pcWvSpORT 6; Site_l: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email: filangdiffetech.com URL: http://fulllength.invitrogen.com.

output

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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full.length cDNA libraries and normalization
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/db_xref="taxon:966"
/db_cxref="taxon:966"
/clone="CSODEOOTYLOZ_PL1"
/clone=lib="LTI_EL002_PL1"
/lab_nost="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville ilianglifetch.com URL:
                                                                                                                                                                                                                                                                       AL541900 B39 bp mRNA linear EST 16-FEB-2001 AL541900 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE007YL07 5 prime , mRNA sequence.
AL541900
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 939)
1 (bases 1 to 939)
1 (bases 1 to 930)
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                                                260 TACAACCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGGTCCAAGAACCAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
                               TACAACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTC
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                                                                                                                                                                                        380 AGTCTCTTATGCTACATTACGTTTGGTGGAAACGTCGCGGGAGCCCT 429
                                                                                                                                                           TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCT 407
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Pred. No. 2.8e-64;
0; Mismatches 48;
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86.0%;
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AUTHORS
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603053578F1 NIH_MGC_122 Homo sapiens cDNA clone IMAGE:5203338 5',
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NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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190 GCCGGGAAGGGACTGGAGTGGATTGGGCGTATAT---ATATAAGTGGGAGCACCAACTAC 246
                                                                                                                                                                                                                                     Gaps
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Email: cgapbs-remail.nlh.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can lette://image.lln.gov

http://image.lln.gov column: 19
                                                                                AACCCGTCCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                       CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCCGTGTATTACTGTGCCAGA----GA
                                                                                                                                                                                                                 TIGGGCCCAAAIAGCIGGAACAACGCIA - - GGCTICIGGGGCCCAGGGAGICCIGGICACC
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0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:5203338"
/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
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/organism="Homo sapiens"
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High quality sequence stop: 797.
Location/Qualiflers
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83.0%;
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Matches 351; Conservative
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BI770055
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/lab host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: BcoR1; cDNA made by oligo-dT priming.
Directionally cloned into BcoR1XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BG684306 680 bp mRNA linear EST 01-MAY-2001 602636046F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4764034 5',
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NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gapbs.rfmail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lln.gov

Plate: LLCM1620 row: k column: 11

High quality sequence stop: 678.
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                                                                           61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                    84
                                                                                                                                                                            25 ATGAAACATCTGTGGTTCTTCCTTCTTCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                                                                                                   CCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC
                                                                                                                                                                                                                                                           259 AACCCTCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCACGTTCTCC
1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                        121 TGCGCTGTCTCTGTGGCGTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/clone="IMAGE:4764034"
/clone_lib="NIH_MGC_48"
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BG684306.1 GI:13915703
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TITLE
JOURNAL
COMMENT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 814)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammallan Gene Collection (MGC)
     οŧ
Hong in the laboratory of Gerald M. Rubin (University or California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
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                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                      ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                                                                                                                                                                                                                                  23 ATGAAACATCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCTGTCCAG
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9
                                                                                                                                                                                                                             Length 680
                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                       Score 285; DB 10;
Pred. No. 1.7e-63;
0; Mismatches 45;
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/db_xref="taxon:9606"
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86.98;
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Similarity
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          /tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: poTB7; Site_1: XhOI;
Site_2: EcoRI; coll made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected 5500bp for average insert size 1.8kb. Library constructed by Ling in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                        Length 814;
                                                                                                                                                                                                                       Score 283.2; DB 10; Length
Pred. No. 5.3e-63;
0; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Ve. Mammalla, Eutheria, Primates, Catarrhini, 1 (bases 1 to 736)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian G. Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
/clone_lib="NIH_MGC_48"
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84.0%;
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BG685592
BG685592.1 GI:
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Matches 358
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/ub.ater="caxon:9900".
/clone="InAGE-1465168"
/clone_lib="NHH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/tlab_host="bluld" (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; CDNA made by oligo-dT priming.
Directionally cloned into ECORIXAhoI sites using the pirectionally cloned into ECORIXAhoI sites using the following 5' adaptor: GGACGAGG(5). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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sapiens cDNA clone IMAGE:5451057 5',
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                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GIGCAGCTGCAAGAGTCGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCTCACC
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CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (
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Pred. No. 1.9e-62;
0; Mismatches 45;
                                                                                                                                           http://image.llnl.gov
Plate: LLCMf633 row: j column: 17
High quality sequence stop: 720.
Location/Qualifiers
                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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603617839F1 NIH_MGC_113 Homo
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85.6%;
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BM008069
BM008069.1 GI:
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EST 24-OCT-2000 5', mRNA
                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Essearch Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
                                                                                                                                                                                                                          Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                                                     AU134293 Linear E AU134293 OVARC1 Homo sapiens CDNA clone OVARC1001672
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1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
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/note="Vector: pME18SFL3"
202 c 169 g 141 t 3
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Pred. No. 2.5e-62;
0; Mismatches 61
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/clone="0VARC100162"
/clone_lib="0VARC1"
                                                                                                              AU134293
AU134293.1 GI:10994832
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 648) NHH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCAGCTGCAGGAGTCGGGCCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 CCA-GGAAGGGGCTGGAGTGGATTGGGAGTGTCTATCATA---GTGGGACGCCTACTACTAC 271
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es 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
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Pred. No. 2.2e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 83.5%;
Matches 355; Conservative
                             Homo sapiens
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                          ORGANISM
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AUTHORS
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446 TCCTCA 451
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ORIGIN
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TITLE
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COMMENT
                                                                                          298
             216
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KEYWORDS
SOURCE
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BG684621
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                                                                                                                                  BG548421 729 bp mRNA linear EST 04-APR-2001 602575006F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4703352 5',
                                                                                                                                                                                                                              Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 729)
                                                                                                                                                                                                                                                                                                                                   Email: cgapbs.remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1541 row: k column: 01
High quality sequence stop: 711.
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NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 280; DB 10;
Pred. No. 3.4e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4703352"
                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                            mRNA sequence. ____BG548421
BG548421 GI:13547086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.2%;
llarity 85.2%;
Conservative
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                                     412 ACCGTCTCCTCA 423
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 570)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMGGO row: n column: 23
High quality sequence stop: 561.
Location/Qualifiers
                                                                                                  273 TACAACCCGTCCTCAAGAGTCGAGTCACCATCTCAGTAGACACGTCCAAGAACCAGTTC 332
                                                                                                                                                                                               133 TCCCTGAAGCTGACGTCTGTGACCCCCGCGGACACGCCCTGTATTATTGTGCGGAGAGA 392
                                                                                                                                                                                                                                                                                                 393 GGCC-----AAGTGGAACGGCGGTGACTACTGGGGCCA-GGAACCCTGGTCACGGT 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
TACAACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTC 297
                                                                                                                                                                      TCCCTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGAT 357
                                                                                                                                                                                                                                                                     TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC 417
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Search completed: September 23, 2002, 17:06:51 Job time: 4510 sec us-09-019-441-2.rng

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September 23, 2002, 17:58:36 ; Search time 488.47 Seconds
(without alignments)
1486.795 Million cell updates/sec
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/ SIDS1/goddata/geneseq/geneseqn_emb1/Na1989.DAT:*
/ SIDS1/goddata/geneseq/geneseqn_emb1/Na1991.DAT:*
/ SIDS1/goddata/geneseq/geneseqn_emb1/Na1992.DAT:*
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1 ATGAAACACCTGTGGTTCTT......TCCTGGTCACCGTCTCCTCA 423
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1736436 segs, 858457221 residues
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                                                                                                                                 OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Anti-human CD23 6G	Primatised anti-hu	Macaque primatized	DNA sequence of a	Nucleotide sequenc	Human damma-4 heav	Human gamma-4E hea	Human gamma-4PE he	Nucleofide sequenc
ΠD	AAV33308	AAT62513	AAV35489	AAS17247	AAZ39331	AAT62868	AAT62869	AAT62870	AAZ39335
DB	19	18	19	24	21	18	18	18	21
% Query Match Length DB ID	423	1431	1431	1431	423	1404	1404	1404	420
% Query Match	100.0	74.0	74.0	74.0	71.2	70.9	70.9	70.9	70.5
Score	423	313.2	313.2	313.2	301.2	299.8	299.8	299.8	298.2
Result No.	т.	7	m	4	S	9	7	80	6

Anti-CD4 VH coding Anti-CD4 cynomolgu Anti-CD4 antibody Monkey anti-CD4 he Human diagnostic a Monkey anti-human Monkey anti-CD4 he Anti-CD4 antibody	Human bladder tumo Human LH11238 mono Primatised anti-hu Macaque primatized DNA sequence of a Human immune syste Human immune syste EST Clone 099. Ho	Human PTHrP monocl Human bladder tumo Human IGFAM-2 immu Vh 71-4. Homo sapi VH411. Homo sapie VH415. Homo sapie VH416. Homo sapie UH416. Homo sapie UH416. Homo sapie Human bladder tumo Human immunoglobul	Monoclonal antibod Human secreted pro Immunoglobulin rB6 F105 rearranged va Human 5 ' EST isola Human 5' EST isola AD26 Homo sapten Human colon cancer Human immunoglobul Functional gamma t
14 AAQ35903 18 AAT91564 19 AAV31428 19 AAV05695 22 AAS03048 18 AAT95167 19 AAV23760			17 AAT18059 22 AAF9947 14 AAC49154 21 AAC49154 21 AAC42134 21 AAC4228 14 AAC42702 18 AAT73440 19 AAV39238
		417 397 746 3348 348 348 348 507	1431 1543 408 426 456 1644 351 393 403
00000000			66 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
2988.2 2988.2 2988.2 298.2 295.2 295.2	9933 992 892	286 281.4 276.2 275.6 275.6 275.6 274 273.6 273.6	272.8 270 269.6 269.6 269.4 269.4 269.2 267.6 266.6
10 11 12 13 14 15 16	22 23 24 25 25 25	26 22 22 33 33 34 34	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3

ALIGNMENTS

AAV33308 standard; DNA; 423 BP

AAV33308;

Anti-human CD23 6G5 moclonal antibody heavy chain variable region DNA. Anti-human CD23 6GS monoclonal antibody; heavy chain variable region; human CD23; 1gS; FCeRii/CD23; gamma-1 constant region; allergy; inflammation; autoimmune disease; allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss. /*tag= a /product= "anti-human CD23 6G5 heavy chain variable region" respon region" /note= "CDS does not contain a stop codon" /*tag= d /note= "encodes CDR 1 region" 208..258 Location/Qualifiers /*tag= b 58..423 /*tag= c 148..165 (first entry) /*tag= Macaca fascicularis 18-NOV-1998 misc_feature misc_feature sig_peptide mat_peptide Key

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WO9640878-A1.
 423
                                                                                                                                                                                                                                                                                                                                    06-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                            07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                            Anderson DR,
                                                                                                           25-MAY-1997
                                                                                                                                                                                                                                                                                                            19-DEC-1996.
421 tca
                                                                                    AAT62513;
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                                                                                                                                                                                                                                                                                                        The present sequence represents a DNA sequence encoding the heavy chain variable region of primate monoclonal antibody anti-human CD23 665. The invention provides primate monoclonal antibodies which specifically bind human CD23, the low affinity receptor for IgE (FCeRii/CD23), and comprise either of a human gamma-1 or human gamma-3 constant region that binds to human FC gamma receptors and inhibits IgE expression. The monoclonal antibodies of the invention are claimed to be useful for inhibiting induced IgE production for treating or preventing allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                           expression to treat or prevent allergic, inflammatory and auto:immune conditions
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                                                                                                                                                                                                                                                                                                                                                                                                                       conjunctivitis, autoimmune haemolytic anaemia, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 423; DB 19; 100.0%; Pred. No. 4.9e-100;
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0
/note= "encodes CDR 2 region"
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                                                                                                                                                                                                                                                                                    Example 1; Pages 104-106; 146pp; English.
                                                                                                                                                                      Reff ME;
                                                                                             98US-0803085.
                                                                      98WO-US02253
                                                                                                                                                                      Nakamura T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 423; Conservative
                                                                                                                                    IDEC-) IDEC PHARM CORP
                                                                                                                                              SEGK ) SEIKAGAKU CORP
                                                                                                                                                                                              WPI; 1998-467495/40.
P-PSDB; AAW70378.
                                                                                                                                                                        Kloetzer WS,
                                                                                             05-FEB-1998;
20-FEB-1997;
                       WO9837099-A1
                                                                      17-FEB-1998;
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                                               27-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Monkey monoclonal antibody binding human 87.1~{\rm or}~87.2 antigen useful for treating autoimmune disease or graft-versus-host disease
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                                                                                                                                                                                   Primatised anti-human B7.1 antigen antibody 16C10 heavy chain DNA.
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                                                                                                                                                                                                                                      Monoclonal antibody; cynomolgus monkey; macaque; 16C10; primatised antibody; B7 antigen; CD28; immunosuppressive; autoimmune disease; idiopathic thrombocytopaenta purpura; systemic lupus erythematosus; rheumatoid arthritis; psorlasis; type i diabetes mellitus; graft versus host disease; hetero-hybridoma; transfectoma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shestowsky WS;
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ВР
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AAT62513 standard; DNA; 1431
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Chimeric Homo sapiens.
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Matches 370; Conserv
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                                                                                                                                                                                                                                                                                                                                CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2; T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine; immunogen; anti-idiotype reagent; interleukin-2; IgG; immunoglobulin G; T cell proliferation; ss.
                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; Mab; macaque; heavy chain; primate; antigen; CD80;
                                                                                                                              405
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                                                                                                 aaccecteceteaagagteaagteaccattteaacagacaegteeaagaaccagttetee 300
                                                                                      CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New monoclonal antibodies specific for B7.1 or B7.2 antigens and inhibiting binding to CD28 - useful as specific immunosuppressants for treating diseases that involve interactions between T and B
                   ------CGCTAGGCTTCTGGGGCCAGGGAGTC
                                                                                                                                         CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACTAC
                                                AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= 16C10 heavy chain
                                                                                                                                                                                                                                                                                                    Macaque primatized 16C10 heavy chain DNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells, e.g. graft rejection or tumours
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1..1431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9819706-A1
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idiopathic thrombocytopaenia purpura, systemic lupus erythematosus, type I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia, inflammatory bowel disease, allergy and multiple sclerosis, graft vs. host diseases, B cell lymphoma, infections (including by human immune deficiency virus) or inflammatory disease and tumours. Optionally the MAD can be conjugated to a drug or toxin. MAD's, or thehr fragments, can also be used as imaging agents and as vaccines or immunogens to develop anti-idiotype reagents. MAD's are optionally combined with other proteins or small molecule immunosuppressants. Blocking B7/CD28 interactions induces long-term, antigen-specific immunosuppression, i.e. it inhibits production of interleukin-2 (IL-2), T cell proliferation and antigen-specific immunoglobulin G (IgG) responses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC 240
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interleukin-2; IL-2; mutant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 313.2; DB 19; Length
Pred. No. 1.6e-71;
0; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
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Best Local Similarity 84.5%;
Matches 370; Conservative (
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Chimeric - Macaca sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAS17247;
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which specifically binds to B7.1 antigen (CDB0) and/or B7.2 antigen (CDB6) for inducting the apoptosis of B7+ cells. The invention is useful for treating diseases such as B cell cancer, lymphoma, a cancer where B cells promote the growth and/or metastasis of tumours, B cell lymphoma, B cell leukaemia, and autoimmune diseases such as idiopathic thrombocytopenia purpura, systemic lupus, erythematosus, type I diabetes mellitus, rheumatora systemic lupus, erythematosus, cype I diabetes mellitus, rheumatora sit attritis, psoriasis, aplastic anaemia, inflammatory bile disease, allergy, multiple sclerosis or graft-vs-host disease. The antibody is useful for immunosuppression in a human or animal and for treating or preventing resistance to or rejection of transplanted disease, for treating reversible obstructive already disease, intestinal inflammations and allergies e.g. Grohn's disease and ulcerative colitis, food-related allergies e.g. migraine, chinitis and eczema, and other types of allergies. The present nucleic side disease and ulcerative disease, so allergies of primatised antibody used in the invention to induce apoptosis and inhibit production of
                                                                                                                                                                                                                                                                                                                                                                                             Use of monoclonal antibody which specifically binds to B7.1 antigen CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells, treating cancer, graft-vs-host disease and autoimmune disease such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tgcgctgtctctggtggctccatcagcggtggttatggctggggctggatccgccagccc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present invention relates to a new use of a monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 24; Length 1431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53; Indels
                                                                      /product- "Heavy chain of 16C10 antibody'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1431 BP; 319 A; 462 C; 385 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 313.2; DB 2
Pred. No. 1.6e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Fig 5b; 89pp; English.
                                                                                                                                                                                                                                                                                                     'n.
                                                                                                                                                                                                                                                                                                       Brams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.0%;
84.5%;
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                                                                                                                                                                                    22-MAY-2001; 2001WO-US16364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 370; Conservative
                                   1..1431
/*tag=
                                                                                                                                                                                                                                                              (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                     Hanna N,
                                                                                                                                                                                                                                                                                                                                         WPI; 2002-089895/12.
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                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAU11646
                                                                                                           WO200189567-A1
                                                                                                                                                                                                                                                                                                   Anderson DR,
                                                                                                                                                29-NOV-2001
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The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antibody, and an acceptor framework from a non-human primate. The Abs are prepared by graftling CDRs from a non-human apecific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
                                                                                                                                                                                                                                                                                                                                                                                                 Complementarity determining region; antibody; primate; immunogenicity; old World ape; Old World monkey; antigen-binding affinity; ss.
aacccctccctcaagagtcaagtcaccatttcaacagacacgtccaagaaccagttctcc 300
                                                                                            405
                                                                                                                        361 cttttttcagttgttggaatggtttacaacaactggttcgatgtctgggggcccgggagtc 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                               CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG
                                              1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GCCCAAATAGCTGGAACAA-------CGCTAGGCTTCTGGGGCCAGGGAGTC
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Pred. No. 1.5e-68;
); Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of Cynomologous VH cDNA clone 2-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 423 BP; 76 A; 125 C; 122 G; 100 T; 0 other;
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                                                                                                                                                                                                                                                                       AAZ39331 standard; DNA; 423 BP
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85.0%;
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                                                                                                                                                                                        421 ctggtcaccgtctcctca 438
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                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                         406 CTGGTCACCGTCTCCA
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca cynomolgus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09955369-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                              CD4; monoclonal antibody; chimaeric antibody; recombinant antibody; cynomolgus monkey; autoimmune disease; rheumatoid arthritis; leukaemia; lymphoma; graft-versus-host disease; asthma;
GCCCAAATAGCTGGAA---CAACGCTAGGCTTCTGGGGGCCAGGGAGTCCTGGTCACCGTC
                                                                                                                                                                                 DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S2 mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human 1964 Fc binding domain framework is
                                            tgcactgtctctggtggctc---cttcagtacttactactggaattggatccgccagccc
                                                             CCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC
                                                                               ccagggaagggactggagtggattggatatatcggtggtggtggtggtcgcccaactac
                                                                                                AACCCGTCCCTCAAGAGTCGAGTCATTTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                   CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGTTGG
                         TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric antibody comprising monkey variable domains and human constant domains - affects CD4-mediated immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                        transplant rejection; HIV; therapy; CE9 gamma 4; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 82-84; 155pp; English.
                                                                                                                                                                                                                                                                        AAT62868 standard; DNA; 1404 BP
                                                                                                                                                                                                                                                                                                                             Human gamma-4 heavy chain DNA.
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                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAW14925
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                                                                                                                                                                                                                                                                                          AAT62868;
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    of
combined with the antigen binding domains (see also AAW14922-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. They can be used to treat autoimmune diseases such as rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAACCTGAACTCTGTGACCGCCGCGCACACGCGTGTATTACTGTGCCAGAGATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 atgaaacacctgtggttcttcctcctcctggtggcagcccccagatgggtcttgtcccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
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                                                                                                                                                                                                                                                               3
                                                                                                                                                                                                                    DB 18; Length 1404;
                                                                                                                                                                                                               Score 299.8; DB 18; Length
Pred. No. 4.5e-68;
0; Mismatches 67; Indels
                                                                                                                                                    Sequence 1404 BP; 312 A; 448 C; 377 G; 267 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human gamma-4E heavy chain DNA.
                                                                                                                                                                                                                    70.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.55
Matches 353; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT62869 standard;
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                                                                                                             arthritis
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9

(first entry)

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Human gamma-4PE heavy chain DNA.
18-OCT-1997
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                                                                                                                                                       DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4E, in which the human IgG4 Fc binding domain framework is combined with the antigen binding domains (see also AAW1492-23) of macague anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat autoimmune diseases such as rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 atattgaaatatcttcactggttattatactggggccagggagtcctggtcaccgtctcc
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                                                                                                                                                                                                                                                                                                                                                                                             .,
m
                                                                     Chimeric antibody comprising monkey variable domains and human constant domains - affects {\rm CD4\text{-}mediated} immune functions, espuseful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                             67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1404 BP; 313 A; 446 C; 379 G; 266 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                   Disclosure; Page 86-88; 155pp; English.
           Reff ME;
                                                                                                                                                                                                                                                                                                                                                                  70.9%;
83.5%;
                                                                                                                                                                                                                                                                                                                                                                                          Matches 353; Conservative
           Newman RA,
                                  WPI; 1997-201913/18
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                               P-PSDB; AAW14926
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tca 420
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                                                                                                           arthritis
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DNA sequences (AAT62868-70) respectively code for the heavy chain regions of human gamma-4 (AAW14925), gamma-4E carrying the L236E mutation (AAW14926) and gamma-4PE (AAW14927) carrying L236E and S229P mutations. They can be used to provide novel monoclonal and chimeric antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4PE, in which the human IgG4 FC binding domain framework is combined with the antigen binding domains (see also AAW14922-23) of macaque anti-human CD4 monoclonal antibody E9.1. These antibodies show high affinity to human CD4, have little or no immunogenicity in humans and show reduced or absence of effector function. The gamma-4E and -4PE mutations confer activity enhanced stability and eliminate depleting activity. The antibodies can be used to treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 gigcagetgeaggagtegggeeeaggactggigaageetteggagaeeetgteeeteaee 120
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CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tgcagtgtctctggtggctccatcagcggtgactattattggttctggatccgccagtcc
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                           cynomolgus monkey; autoimmune disease; rheumatold arthritis;
leukaemia; lymphoma; graft-versus-host disease; asthma;
transplant rejection; HIV; therapy; CE9 gamma-4PE; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric antibody comprising monkey variable domains and hum constant domains - affects CD4-mediated immune functions, e useful for treatment of autoimmune disease, e.g. rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1404 BP; 313 A; 447 C; 379 G; 265 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eliminate depleting activity. The antibodies ca
autoimmune diseases such as rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70.9%; Score 299.8; DB 1
ilarity 83.5%; Pred. No. 4.5e-68;
Conservative 0; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 91-93; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reff ME;
                                                                                                                                                                                                                                                                                                                             96WO-US14324.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1997-201913/18
P-PSDB; AAW14927.
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Best Local Similarity
Matches 353; Conserv
                                                                                                                                                                                                        WO9709351-A1.
                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                             05-SEP-1996;
                                                                                                                                                                                                                                                                   13-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hanna N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis
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AAT62870 standard; DNA; 1404

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AAT62870 RESULT

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AAT62870;

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gttcaactacaggagtcgggcccaggactgatgaagccttcggagacctgtccctcacc 120
                                                                       CTGAACCTGAACTCTGTGACCGCGCGCACACGCGCGTGTATACTGTGCCAGAGATTGG
                                                                                                                                                                                                 CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACTAC
                    TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
                                                                                                      AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                  ctgagactgacctctgtgaccgccgcggacacggccgtttattactgtgcgagagat---
                                                                                                                                                                                        GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                                                                                          AAQ35903 standard; DNA; 423 BP.
                                                                                                                                                                                                                                                                                                                                                                      Anti-CD4 VH coding sequence.
                                                                                                                                                                                                                                                     tca 420
                                                                                                                                                                                                                                 TCA 423
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                                                                                                                                                                                                                                                                                                                            AAQ35903;
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61
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                                                                                                                                                                                                                                                                                                                                The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigenspecific donor antibody onto homologous Old World ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in
                                                                                                                                                                                                                                                     Complementarity determining region; antibody; primate; immunogenicity; Old World ape; Old World monkey; antigen-binding affinity; ss.
                             357
                                                  420
                                                             in humans (because of the close similarity between the human and prin
proteins), but retain the full antigen-binding affinity of the donor
                   CTGAACCTGAACTCTGTGACCGCGCGCGCACGCCGTGTATTACTGTGCCAGAGATTGG
                                                  GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                                                                                                Nucleotide sequence of Cynomologous VH cDNA clone 2-10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 420 BP; 80 A; 125 C; 113 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 84-85; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                  BP.
                                                                                                                                                                 AAZ39335 standard; DNA; 420
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                                                                                                                                                                                                                                                                                                                                                                      98US-0083367
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P-PSDB; AAY56667, AAY56732.
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                     Macaca cynomolgus.
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tca 420
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                                                                                          TCA 423
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                                                                                                                                                                                                                                                                                                                                                                                                              Taylor AH;
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(first entry)

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The sequences given in AAQ35903-04 encode the Simian anti CD4 VH and V-lambda sequences respectively. These sequences were derived using the primer sequences given in AAQ35901-02. The amplification products were sequentially cloned into the vector TCAE 6, which contains human IGC1 and human lambda constant regions. The amplified sequences could be used in the production of a recombinant antibody, comprising a
PCR; amplify; clone; heavy; light; chain; variable; region; lambda; immortalised B-cell; vector; TCAE 6; human; igG1; constant; antigen; recombinant; antibody; chimpanzee; Ig; Ag; old world monkey; eczema; immunoglobulin; therapeutic; rheumatoid arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant antibodies including Old World monkey portion and human portion - used for treatment of auto-immune diseases, infectious diseases, AIDS, tumours, diabetes, proliferative diseases, intestinal inflammations and allergies, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 53-54; 92pp; English.
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92US-0856281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IDEC-) IDEC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hanna N, Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1993-058729/07.
P-PSDB; AAR31948.
                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-1992;
                                                                                                                                                                                                                                                                   WO9302108-A.
                                                                                                                                                                                                                                                                                                                                          04-FEB-1993
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DB 21; Length 420; Indels

70.5%; Score 298.2; DB 21; llarity 83.2%; Pred. No. 8.9e-68; Conservative 0; Mismatches 68;

al Similarity 352; Conserv

Query Match Best Local S

Matches

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CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120

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91US-0735064

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25-JUL-1991;
                                                                               Hanna N,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region.
                                                                                                        Gaps
        region and an antigen (Ag) binding portion of an old world monkey Ig varible region, where the old world monkeys may be the same or different. The recombinant antibody may be used as a therapeutic agent for the treatment of rheumatoid arthritis, eczema and
                                                                                                                        9
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chimpanzee or old world monkey immunoglobulin (Ig) constant
                                                                                                                                                                                                                                       ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                   CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                   TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
                                                                                                                                                                                                             tgcagtgtctctggtggctccatcagcggtgactattattggttctggatccgccagtcc
                                                                                                                                                                                                                                                                AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACCACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                                                   CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATTGG
                                                                                                                                                                                                                              CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC
                                                                                                                                                                                                                                                                                                                                      GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACÇGTCTCC
                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig; chimpanzee; chimeric antibody; human therapy; Old World monkey;
                                                                                                        Indels
                                                            Seguence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                     DB 14;
                                                                               Score 298.2; DB 14;
Pred. No. 8.9e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= Anti-CD4_VH_region
/note= "No stop codon given"
                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT91564 standard; DNA; 423 BP.
                                                                                     Query Match 70.5%;
Best Local Similarity 83.2%;
Matches 352; Conservative
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                                           immunological disorders.
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/*tag=
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tca 423
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                                                                                      Query Match
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chimpanzee immunoglobulin (ig) constant region and an old world monkey an antigen (Ag)-binding region. The present sequence encodes an anti-CD4 cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody (Ab) comprising the light and heavy chain variable regions encoded by the present sequence and that of AAM91555 is also new. The Abs are useful for human therapy, especially of tumours. Old world monkeys are sufficiently different from humans to allow Abs against human Ags, even relatively conserved Ags such as CD4 and CD54, to be raised in these monkeys, and are sufficiently similar to humans to avoid host anti-Ab immune responses when the Abs are introduced into humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a human or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 gtgcagctgcaggaggcggggcccaggactggtgaagccttcggagaccctgtccctcacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 ccagggaagggactggagtggatcggctacatctatggcagtggtggggggcaccaattac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACAGGTCCAAGAACCAGTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCAGGGAGTCCTGGTCACGTCTCC
                                                                                                                                                                                                                                                                                                                                                 Chimeric antibodies for human therapy - comprising human or chimpanzee immunoglobulin constant region and an Old World monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chimeric antibody (Ab) has been developed comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.5%; Score 298.2; DB 18;
llarity 83.2%; Pred. No. 8.9e-68;
Conservative 0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 33; Fig 13; 46pp; English.
                                                                                                                                                                                                          RW;
92US-0912292.
91US-0735064.
92US-0856281.
95US-0379072.
                                                                                                                                                                                                          Raab
                                                                                                                                                PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                           antigen-binding region
                                                                                                                                                                                                          Newman RA,
                                                                                                                                                                                                                                                                WPI; 1997-424183/39
P-PSDB; AAW32477.
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nes 352; Conserv
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   10-JUL-1992;
                                 25-JUL-1991;
                                                         23-MAR-1992;
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CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCAGAGATTGG 360
184 ccagggaagggactggagtggatcggctacatctatggcagtggtggggggaccaattac 243
                                        AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                          ctgaaactgaggtctgtgaccgccgggacacggccgtctattactgtgcgagtaat---
                                                                                                                                   GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCC
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/product=
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61..420
/*tag= 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                   tumour; antibody; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1998-031820/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Macaca cynomolgus.
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                                                                                                                                                                                                                423
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23-MAR-1992;
25-JAN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                      05-MAY-1998
                                                                                                                                                                                       TCA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5693780-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
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                                                                                                                                                                                                       AAV05695;
                                                                                                                                                                                                                                                         RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This DNA encodes the heavy chain variable region (VH) of the cynomolgus monkey anti-CD4 antibody. The antibody comprises antigen-binding sequences from an old World monkey antibody and human constant domain sequences. The antibody specifically binds to CD4 and can be used in the treatment of rheumatoid or psoriatic arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCAGGGAAGGGACTGGAGTTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACTAC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 gtgcagctgcaggaggcgggcccaggactggtgaagccttcggaagaccctgtccctcacc 123
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/transl_except= (pos:415..417, aa:Ser)
/product= "Variable heavy chain antigen binding
                                                                                                                    Anti-CD4 antibody; antigen-binding; treatment; chimeric; human; monkey; rheumatoid arthritis; psoriatic arthritis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 298.2; DB 19; Length 423; Pred. No. 8.9e-68; 0; Mismatches 68; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises
                                                                                           Anti-CD4 antibody variable heavy (VH) region encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of rheumatoid and psoriatic arthritis · comprise administration of chimeric human-monkey anti-CD4 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Columns 35-36; 47pp; English.
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raab RW;
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83.2%;
                                                                                                                                                           - Macaca cynomolgus.
- Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                         95US-0476237.
91US-0735064.
92US-0856281.
92US-0912292.
95US-0379072.
           AAV31428 standard; DNA; 423
                                                                                                                                                                                                                                                                                                                                                   95US-0476237
                                                                (first entry)
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Best Local Similarity 83.2%
Matches 352; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IDEC-) IDEC PHARM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newman RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-321461/28.
P-PSDB; AAW57446.
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23-MAR-1992;
10-JUL-1992;
                                                                10-AUG-1998
                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                              US5756096-A.
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                                                                                                                                                                                                                                                                                                                        26-MAY-1998
                                                                                                                                                           Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanna N,
                                    AAV31428;
                                                                                                                  Anti-CD4
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Primer; PCR; amplification; leader sequence; human; monkey; baboon; macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid; lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
                                                                                                                                                                                          /product= "Ig heavy chain variable region"
/note= "no stop codon given at the 3' end of sequence"
4..60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the coding sequence for the heavy chain variable region from an anti-human CD4 immunoglobulin raised in cynomolgus monkeys. The sequence was PCR amplified and used in the
                                                                  Monkey anti-CD4 heavy chain variable region coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid encoding hybrid antibody - comprising monkey antigen-binding region and human or chimp constant region
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; Fig 13; 46pp; English
AAV05695 standard; DNA; 423 BP.
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910S-0735064.
920S-0856281.
950S-0379072.
950S-0481869.
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construction of a recombinant antibody comprising: (i) an Old World monkey Ig antigen-binding region; and (ii) a human or chimpanzee Ig constant region. The hybrid antibodies can be used as passive or active therapeutic against human diseases, e.g. B-cell lymphoma, AIDS, autoimmune and inflammatory diseases, transplant rejection or tumours, or for producing therapeutic and diagnostic conjugates. Although evolutionary distant monkeys are used to raise antibodies against human antigens, they are sufficiently similar that they produce antibodies similar to human antibodies, such that when the monkey antibodies are introduced into humans, no host anti-antibody response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                                                                                                                                                                                                    4 atgaaacacctgtggttcttcctcctctggtggcagcccccagatgggtcttgtcccag
                                                                                                                                                                                                                                                                                                                                                                     61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC
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                                                                                                                                                                                                                                            Length 423;
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                                                                                                                                                                                                                                                                         68; Indels
                                                                                                                                                                                            Sequence 423 BP; 85 A; 122 C; 113 G; 103 T; 0 other;
                                                                                                                                                                                                                                          DB 19;
                                                                                                                                                                                                                                          Score 298.2; DB 1
Pred. No. 8.9e-68;
                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                        70.5%;
83.2%;
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                                                                                                                                                                                                                                                         Similarity
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tca 423
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                                                                                                                                                                                                                                          Query Match
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The present sequence for human diagnostic and therapeutic (dithp) cDNA sequence #37 is 1 of 71 (AAS03012-AAS03082) novel sequences described in the invention. The present sequence (Incyte ID No: 4442487dec) encodes an antigen recognition molecule. The dithp polynucleotides may be used to diagnose a condition disease or disorder associated with human molecules. They can be used to identify the presence of similar nucleic acids. Dithp polynucleotides may used to generate hybridisation probes for use in chromosomal mapping. Polypeptides (DITHP) encoded by dithp are used to screen for molecules which bind to them and modulate their activity. Dithp polynucleotides can be used for gene therapy of disorders such as severe combined immunodeficiency syndrome (SCID).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infectious disorders and developmental disorders. The antibodies can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cystic fibrosis, thalassemia, haemophilia resulting from Factor VIII or IX deficiencies, cardiovascular disorders e.g familial hypercholesterolaemia (FH), cell proliferative disorders e.g. cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stockdreher TK:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
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                                                                                                                                                                                                                                                                                                                                                                                                  Banville SC;
Shah P, Chalup MS;
Panzer SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel diagnostic and therapeutic polynucleotides, used in disease diagnosis and for gene therapy of conditions such as cancer and thalassemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGAAACACCTGTGGTTCTTCCTCCTCGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurodegenerative disorders, autoimmune/inflammatory disorders,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 619;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                 Dufour GE, Cohen HJ, Rosen BH,
Jones AL, Yu JY, Greenawalt LB,
, Wright RJ, Chen W, Liu TF, Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.1%; Score 296.4; DB 2
84.3%; Pred. No. 2.8e-67;
                                                                                                                                                                                                                                                                                                                                                                                                      Spiro
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Dufour GE, Cohen HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 273; 299pp; English.
                                                                                                                                                                                      990S-0167520.
990S-0167542.
990S-0167943.
990S-0167945.
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990S-0168429.
990S-0168432.
990S-0168468.
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99US-0156625.
99US-0167410.
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             2000WO-US25643
                                                            99US-0155939
99US-0156294
                                                                                             99US-0156565
                                                                                                                                                                                                                                                                                                                                                                    (INCY-) INCYTE GENOMICS INC
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             19-SEP-2000;
                                                                                          28-SEP-1999;
                                                                                                                                                                                         24-NOV-1999;
                                                                                                                                                                                                       24 - NOV - 1999;
                                                                                                                                                                                                                                     29-NOV-1999;
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Hillman JL,
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                                                                     AACCCGTCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
                                                                               357
                                                                                                                                                              ctgaagctgagctctgtgaccgccgcggacacggccgtgtattactgtgcgactttctac 392
                                                                                                                                                                                                                                                                                                                                                                                        vaccine; immunogen, immunotherapy; anti-idiotypic response; immunosuppression; treatment; prevention; proliferative disease; hyperproliferative disease; immunologically mediated disease; rheumatoid arthitis; lugus erythematosus; SLE; Hashimoto's thyroiditis; systemic lugus erythematosus; SLE; Hashimoto's thyroiditis; multiple solerosis; myasthenia gravis; type 1 diabetes; uveitis; nephrotic syndrome; psoriasis; atopical dermatitis; contact dermatitis; exematous dermatitides; seborrheic dermatitis; Lichen planus; Pemplugus; bullous pemphigus; Epidermolysis bullosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cutaneous eosinophilia; alopecia areata; reversible obstructive airways disease; intestinal inflammation; intestinal allergy; Coeliac disease; proctitis; eosinophilia; gastroenteritis; mastocytosis; Crohn's disease; ulcerative colitis; food related allergy; migraine; rhinitis; eczema:
                                      CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCGTGTATTACTGTGCCA---GAGAT
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                             CCAGGGAAGGGACTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC
                                                                                                                                                   TGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTC
                                                                                                                                                                                                                                                                                                                              Monkey anti-human CD4 antibody heavy chain variable region cDNA
                                                                                                                                                                                                                                                                                                                                                            variable region; chimeric antibody; B cell lymphoma; infectious disease; AIDS; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                inflammatory disease; transplant rejection; imaging reagent;
                                                                                                                       immunoglobulin; Ig; heavy chain; CD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related allergy; migraine; rhinitis; eczema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   urticaria; angioedemas; vasculitides; erythema;
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Location/Qualifiers
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/note= "stop
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tcctca 458
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The present sequence encodes a monkey anti-human CD4 antibody heavy chain variable region, which was used in the development of a novel method for producing a chimeric antibody (Ab), comprising the variable region of an Old World monkey (OWM) Ab and the constant region of a human Ab. The method comprises amplifying DNA from the OWM using a primer complementary to the 5' leader sequence of the OWM who gene and fusing the resulting variable region coding sequence with a human constant region coding sequence with a human constant region coding sequence with a human constant region coding sequence. The chimeric Ab may be used as a passive or active therapeutic for B cell lymphoma, infectious, e.g. ADS, autoimmune and inflammatory diseases and transplant rejection. The Ab can be used in its native form or as part of an Ab/chelate, Ab/drug or Ab/toxin complex.

Additionally, a whole Ab, or a fragment (Fab2, Fab, Fv) may be used as an imaging reagent or as a potential vaccine or immunogen in active immunotherapy to generate anti-idictypic responses.

An anti-CD4 recombinant Ab, or a fragment can also be used to induce immunosupression and can therefore be used to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of humanised antibodies containing monkey variable region - used for the treatment of B cell lymphoma, autoimmune disease, inflammatory disease and infection, e.g. by HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erythema, cutaneous eosinophilias, alopecia areata), reversible obstructive airways disease, intestinal inflammations and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Ab of the invention is non-immunogenic and therefore does
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            induce a human anti-Ab response. It also has a relatively lo
half-life and a full effector function with human cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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Pred. No. 5.3e-67;
0; Mismatches 68;
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91US-0735064.
92US-0856281.
95US-0379072.
95US-0478039.
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Best Local Similarity 83.1%;
Matches 349; Conservative (
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                                                23-MAR-1992;
25-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eczema)
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Search completed: September 23, 2002, 17:58:42 Job time: 7006 sec

Run on:

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ATGAAACACCTGTGGTTCTT.....TCCTGGTCACCGTCTCCTCA 423
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cgn2_6/ptodata1//pna/US095_COMB.seq;*
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                      21979536 seqs, 10817449327 residues
                                                                                                                                                                                                                                                                                                                                                                                                                  hits satisfying chosen parameters:
                                                                                                                              September 23, 2002, 19:47:11
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Maximum Match 100%
Listing first 45 summaries
                                                                                  - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                             Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Database

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/ptodata/1/pna/US6034_COMB.seq
/ptodata/1/pna/US6035_COMB.seq
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description
SUMMARIES			ID
			e Match Length DB]
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			Score

Length DB

Description Sequence Seguence Sequence

Sequence 709, App Sequence 7148, Ap Sequence 40, Appl

Sequence 420,

Sequence 1

Sequence 40, Sequence 40, Sequence 7, A

1 US-09-019-441-2 1 US-09-292-053-3 1 US-08-292-053-3 1 US-09-383-916-11 2 US-09-576-424-11 2 US-09-562-484-11 2 US-09-60131-40 1 US-09-824-559-7148 1 US-09-824-559-7148 1 US-09-612-914-7 1 US-09-612-914-7 2 US-09-612-914-7 3 US-09-612-914-7 3 US-09-612-914-11 4 US-09-612-914A-1 5 US-09-612-914A-1 6 US-09-612-914A-1 7 US-09-612-914A-1 8 US-09-612-914A-1 8 US-09-612-914A-1 9 US-09-612-914A-1 1 US-09-612-914A-1

Sequence 9, Sequence 11,

Sequence 505, App Sequence 23569, A Sequence 23569, A Sequence 23569, A

US-60-168-599-505 US-09-362-510-23569 US-09-362-510A-23569 US-09-904-013-23569 US-09-612-914-1

Sequence 1 Sequence 1 Sequence 1

US-09-612-914A-1 US-09-203-768A-1 US-09-989-901-1

Sequence

Sequence 44, Appl Sequence 44, Appl Sequence 44, Appl

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Sequence 15, Sequence 15, Sequence 15,

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Sequence 7

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APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: NAKAWIRA, TAKEHIKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
TITLE OF INVENTION: THEREOF AS THERAPEUTICS
FILE REFERENCE: 23522 06699
CURRENT APPLICATION NUMBER: US/09/292,053
CURRENT FILING DAFF: 1999-04-14
PRIOR FILING DAFE: 1999-04-14
                                                                                                                           61 CIGCAGCIGCAGGAGICGGGCCCAGGAGIGGIGAAGCCIICGGAGACCCIGICCCICACC 120
                                                                                                                                                                    121 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
                                                                                                                                                                                   CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACTAC 240
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                          Gaps
                                                    ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCTCCCCAGATGGGTCCTGTCCCAG 60
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                                                                                                                                                                                                                                         241 AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGAACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                                 AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
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                          Indels
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           Pred. No. 1.3e-96;
Mismatches 0;
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Pred. No. 1.3e-96;
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100.0%; Pred. No. ...
0; Mismatches
100.08; Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09292053 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 423; Conservative
                        423; Conservative
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NAME/KEY: sig_peptide
LOCATION: (1)..(58)
NAME/KEY: mat_peptide
'OCATION: (58)..(423)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 423
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIN Ve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(423)
US-09-292-053-3
          Best Local Similarity
Matches 423; Conserv
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                                                Sequence 5770, Ap Sequence 1935, Ap Sequence 2, Appli Sequence 164, App Sequence 708, App Sequence 16228, A Sequence 6, Appli A
                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09019441
GENERAL INFORMATION:
GENERAL INFORMATION:
KLOETZER, William S.
NAKAWORA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                       Sequence
             Sequence
                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 423;
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                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS,
STREET: P.O. BOX 1404
                                                US-09-710-281-5770
US-09-726-172-1935 US-09-726-172-1935 US-09-604-897-164
US-09-665-486-418
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US-09-340-623-16228
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US-09-998-8888-16228
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PRIOR APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGBNT INFORMATION:
NAME: TESKIN, RObin L.
REGISTRATION NUMBER: 35,030
REFERENCE/COCKET NUMBER: 012712-50:
TELEPHONE: (703) 836-6620
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   012712-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                      ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-019-441-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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58..423
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MOLECULE TYPE: DNA (genomic)
FEATURE:
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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          FEATURE
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Gaps

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APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHRAMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSS:
                                                                                                                                                                                                                                                                                                                                                                                    241 AACCCTCCCTCAAGAGTCAAGTCACCATTCAACAGACACGTCCAAGAACCAGTTCTCC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CIGCAGCIGCAGGAGICGGGCCCAGGAGIGGIGAAGCCIICGGAGACCCIGICCCICACC 120
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                                                                                                          Length 1431;
                                                                                                                                            Indels
                                                                                                            DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                            53;
                                                                                                          Score 313.2; DB 1
Pred. No. 9.1e-69;
); Mismatches 53
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                               74.0%; Scur.
84.5%; Pred
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DNA (genomic)
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                                                                                                            Query Match
Best Local Similarity
 MOLECULE TYPE:
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                               NAME/KEY:
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                                              ; LOCATION:
US-08-746-361-6
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                                                                                                                                            Matches 370;
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APPLICANT: HANNA, Nabil
APPLICANT: HANNA, Nabil
APPLICANT: BRAMS, Peter
TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
TITLE OF INVENTION: INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
TITLE OF INVENTION: AND B7.2 CO-STIMULATORY ANTIGENS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                            CCAGGGAAGGGACTGGATTGGACGTATCTCTCGTAGTGGTGGGGCCCACCAACTAC
                                                                                                                                                                                                                                                                         CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG
                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BURNS, DONNE, SWECKER & MATHIS STREET: P.O. Box 1404
CITY: Alexandria STAFE: Virginia COUNTRY: United States ZIP: 22313-1404
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 1431 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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PRIOR APPLICATION NUMBER: PCT/US97/19906
PRIOR FILING DATE: 1997-10-29
PRIOR PLICATION NUMBER: 08/746,361
PRIOR PLICATION NUMBER: 08/487,550
PRIOR PLICATION NUMBER: 08/487,550
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11
LENGTH: 1431
 2000-05-22
                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                            ; LOCATION: (1)..(1428)
US-09-576-424-11
   CURRENT FILING DATE:
                                                                                                                                                                                                                             NAME/KEY: CDS
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APPLICANT:
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GENERAL INFORMATION:
APPLICANT: ANDERSON MABIL
APPLICANT: HANNA, NABIL
APPLICANT: HANNA, CHERLER
APPLICANT: HEARNS, PETER
APPLICANT: HEARNS, CHERLER
TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
FILE REPERENCE: 37003-275661
CURRENT APPLICATION NUMBER: US/09/576,424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 AACCCTCCCTCAAGAGTCAAGATTACAACAGACAGGTCCAAGAACCAGTTCTCC 300
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                                                                                                                                                                                                                                                                                                                                                                          Length 1431;
                                                                                                                                                                                                                                                                                                                                                                           Score 313.2; DB 17; Length
Pred. No. 9.1e-69;
0; Mismatches 53; Indels
                                                 012712-131
               NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                           INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 1431 base pairs TYPE: nucleic acid STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.0%;
Best Local Similarity 84.5%;
Matches 370; Conservative
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
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LOCATION: 1..1
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US-09-383-916-11
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US-09-576-424-11
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                                             Gaps
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                                                                                                                                                                                                                                                                            121 TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGTGGACCTGGATCCGCCAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                               241 AACCCGTCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 GCCCAAATAGCTGGAACAA-------CGCTAGGCTTCTGGGGCCAGGGAGTC
                                             15;
  DB 22; Length 1431;
                                             Indels
Score 313.2; DB 22;
Pred. No. 9.1e-69;
0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-665-486-420; Sequence 420, Application US/09665486; GENERAL INFORMATION:
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Chalup, Michael S.
Hillman, Jennifer L.
Jones, Anissa L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lincoln, Stephen E. Russo, Frank D. Spiro, Peter A. Banville, Steve C. Bratcher, Shawn R.
Query Match 74.0%;
Best Local Similarity 84.5%;
Matches 370; Conservative 0
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Cohen, Howard J.
Rosen, Bruce H.
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Lincoln, Stephe
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493
434 atggttcggggagggttcagctggttcgaccctgggggccagggaaccctggtcactgtc 493
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Fong, Willy Tuen
                                                                                                                                                                                                  Jones, Anissa L.
Yu, Jimmy Y.
                                                                                                                                                                                                                                                   Panzer, Scott R.
Roseberry, Ann M.
Wright, Rachel J.
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Liu, Tommy
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                                                                                                                                                                                                                                                                                                                                               Yap, Pierre E
                                                                                                                                                                                                                              APPLICANT RUSSO, Frank D.
APPLICANT RUSSO, Frank D.
APPLICANT RUSSO, Frank D.
APPLICANT Banville, Steve C.
APPLICANT Bratcher, Shawn R.
APPLICANT Bratcher, Shawn R.
APPLICANT Cohen, Howard J.
APPLICANT ROSEN, Bruce
APPLICANT HILLMAN, Jennifer L.
TITLE OF INVENTION ANTIGEN RECOGNITION MOLECULES
FILE REFRENCE: PT-0099 P.
CURRENT APPLICATION NUMBER: US/60/168,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 304.4; DB 55;
Pred. No. 1.4e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 444854.24
; 566-168-599-709
                                                                                                                                                              Sequence 709, Application US/60168599 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 72.0%;
Best Local Similarity 85.4%;
Matches 364; Conservative
                                                                                                                                                                                                  APPLICANT: Hodgson, David M. APPLICANT: Lincoln, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 737
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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                                    418 TCCTCA 423
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tcctca 499
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US-60-168-599-709
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Pred. No. 1.4e-66;
0; Mismatches 56;
                                                                                                                                                            APPLICANT: Amshey, Stefan
PPLLICANT: Fong, Willy T.
TILLE OF INVENTION: ANTIGEN RECOGNITION MOLECULES
FILE REFERENCE: PT-0076 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature; OTHER INFORMATION: Incyte ID No: 444854.24.dec
US-09-665-486-420
                                                                                                                                                                                                                         FILE KEFEKENES: PT-U076 US
CURRENT APPLICATION NUMBER: US/09/665,486
CURRENT FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 60/156,297
PRIOR FILING DATE: 1999-09-24
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-8
PRIOR PELING DATE: 1999-09-8
PRIOR PELING DATE: 1999-09-8
PRIOR PELING DATE: 1999-12-01
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-11-30
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/168,613
PRIOR FILING DATE: 1999-12-02
                                                                                   Chen, Wensheng
Liu, Tommy F.
Yap, Pierre E.
Stockdreher, Theresa K.
Amshey, Stefan
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85.4%;
                                                   Roseberry, Ann M. Wright, Rachel J.
                                  Panzer, Scott R.
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PERL Program SEQ ID NO 420 LENGTH: 681
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NUMBER OF SEQ ID NOS:
                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
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GRNERAL INFORMATION:
APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770
CURRENT FILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-04-28
PRIOR FILING DATE: 1998-04-28
                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                  Score 301.2; DB 1
Pred. No. 8.2e-66;
0; Mismatches 58
                FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: PCT/US99/09131
CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 60/083,367
EARLIER FILING DATE: 1998-04-28
SOFTWARE: FSEC ID NOS: 97
SOFTWARE: FASTSEQ for Windows Version 3.0
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    IITLE OF INVENTION: Immunogenicity
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85.0%;
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Best Local Similarity 85.0
Matches 362; Conservative
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SOFTWARE: FastSEQ for
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; LOCATION: (1).
PCT-US99-09131-40
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LENGTH: 423
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LENGTH: 423
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                                                                                                                                               APPLICANT: Holtzman, Douglas A.
APPLICANT: Holtzman, Douglas A.
APPLICANT: Jakubowski, Joseph A.
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREFOR
ETLE REFERENCE: 1600.2077-001
CURRENT PRILING DATE: 2001-04-02
PRIOR PILING DATE: 2001-04-02
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 9929
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PCT-US99-09131-40
; Sequence 40, Application PC/TUS9909131
; GENERAL INFORMATION:
; APPLICAMY: Taylor, Alexander H
; TITLE OF INVENTION: Monoclonal Antibodies with Reduced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 303.2; DB 31;
Pred. No. 2.7e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                           Sequence 7148, Application US/09824559 GENERAL INFORMATION: APPLICANT: Gearing, David P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)...(541); OTHER INFORMATION: n = A,T,C or G US-09-824-559-7148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 71.7%;
Best Local Similarity 87.0%;
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  494 tcctca 499
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SNGTH: 541
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                                                         238 aattootootoaagagtogoatoacoctgtoactagaogogtocaagaaocagttotoo
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                                                                                                                TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGTGGACCTGGATCCGCCAGCCC
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 1 atgaagcacctgtggttcttcctcctcctggtggcagctcctagatgggtcctgtcccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human TITLE OF INVENTION: Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/612.914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 10-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JMBER: US/09/612,914
10-JUL-2000
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentr Pr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09612914 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hanna, Nabil
APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1404 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
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EDNESS: single
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STRANDEDNESS:
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                                                                                                                Length 423;
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Taylor, Alexander H
TITLE OF INVENTION: Monoclonal Antibodies with Reduced
TITLE OF INVENTION: Immunogenicity
FILE REFERENCE: P50770
CURRENT APPLICATION NUMBER: US/09/905,243
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/300,970
PRIOR FILING DATE: 1999-04-28
                                                                                                                DB 17;
                                                                                                              Score 301.2; DB 1
Pred. No. 8.2e-66;
                                                                                                                                                  0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                              71.2%;
85.0%;
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                                                                                                          Query Match
Best Local Similarity 85.0
Matches 362; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 85.0
Matches 362; Conservative
               ; NAME/KEY: CDS
; LOCATION: (1)...(423)
US-09-300-970A-40
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; LOCATION: (1)...(423)
US-09-905-243-40
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tcttca 423
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LENGTH: 423
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FEATURE:
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RESULT 14
US-09-612-914-11
; Sequence 11, Application US/09612914
                                                                                                     NAME: TESKIN, RODIN L. REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 015 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
              FILING DATE: 10-JUL-2000
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.9%;
83.5%;
                                                                                                                                                                  TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEO ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                  1404 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.59
Matches 353; Conservative
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POSITION IN GENOME:
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TCA 420
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; LOCATION:
US-09-612-914-9
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FEATURE:
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GENERAL INFORMATION:
HADDAT: Hanna, Nabil
APPLICANT: Hanna, Roland A.
APPLICANT: Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNA, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                            heavy chain variable and constant gamma
                                                                                                                                                                                                  Length 1404
                                                                                                                                                                                                                               67; Indels
                                                                                                                                                                                                 DB 23;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                 Pred. No. 2.2e-65;
                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                  Score 299.8;
DNA (genomic)
                                                                                                                                                                                               70.9%;
83.5%;
                                                                                                                                                                                                               Best_Local Similarity 83.5
Matches 353; Conservative
                                                                                                                       mat_peptide
1..1404
           POSITION IN GENOME:
CHROMOSOME/SEGMENT:
CHROMOSOME/SEGMENT:
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CITY: Alexandria
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                                                        FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                   ; NAME/KEY;
; LOCATION:
US-09-612-914-7
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Pred. No. 2.2e-65
0; Mismatches 65
US/08/523,894
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AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
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          APPLICANT: Newman, Roland A.
APPLICANT: Reff. Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
TITLE OF INVENTION: Therapy
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23; Length 1404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain gamma 4 with the P and
                                                                                                                                                 STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.9%; Score 299.8; DB 23;
83.5%; Pred. No. 2.2e-65;
ive 0; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                              PRICE APPLICATION DATA:
APPLICATION NUMBER: US/08/523,894
FILING DATE: 06.5EP-1955
ATTONNEY/GENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-620
TELEPHONE: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
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STRANDEDNESS: single
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CHROMOSOME/SEGMENT:
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Best Local Similarity
Matches 353; Conserv
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FEATURE:
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US-09-612-914-11
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241 AATCCCTCCTCAACAACAATGGAGTCTCCATTTCAATAGACAGGTCCAAGAACCTCTTCTCC 300 CTGAACCTGAACTCTGTGACCGCCGCGGACACGCCCGTGTATTACTGTGCCAGAGATTGG 360 361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 420 358 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 417 CHROMOSOME/SEGMENT: heavy chain variable and constant gamma Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy Version #1.30 CORRESPONDENCE ADDRESS: ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS STREET: 699 Prince Street COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995 NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION: ; LOCATION: 1..1404 ; SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-09-612-914A-7 Sequence 7, Application US/09612914A GENERAL INFORMATION: COUNTRY: USA ZIP: 22314-3187 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY disk TELEPHONE: 703-836-6620 TELEFAX: 703-836-2021 LENGTH: 1404 base pairs TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) POSITION IN GENOME:

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                                       Gaps
Ouery Match 70.9%; Score 299.8; DB 23; Length 1404; Best Local Similarity 83.5%; Pred. No. 2.2e-65; Matches 353; Conservative 0; Mismatches 67; Indels 3;
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Search completed: September 23, 2002, 19:47:18 Job time: 7013 sec

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2056.838 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGAAACACCTGTGGTTCTT......TCCTGGTCACCGTCTCCTCA 423
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Sequence 190,
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USO0_NEW_COMB.seq:*
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-971-631-11
US-10-124-807-11
US-10-124-805-11
US-10-130-390-11
US-10-211-357-7
US-10-211-357-7
US-09-850-165-15
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US-10-206-008-190
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Maximum Match 100%
Listing first 45 summaries

    nucleic search, using sw model

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Maximum DB seq length: 200000000
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6460, AP
20932, A
20398, A
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13582, A
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21, Appl
114467,
             21, Appl
16699, A
                                13, Appl
16650, A
4, Appli
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35, Appl
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ALIGNMENTS

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GENERAL INFORMATION:
Sequence 2, Application US/10103686
INTERPORTER NITE OF INVENTION: GAMANIA . ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: GAMANIA . ANTI-HUMAN CD23 MONOCLONAL
MANDRER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSED: BURNS, DOARE, SWECKER & MATHIS
STREET: P.O. Box 1404
CONTRY: Uliquia
STRIE: P.O. Box 1404
COMPUTE READABLE FORM:
MEDIUM TYPE: IDPROPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: IDPROPY GONDELINE
SOFTWARE: PATENTION RELEASE
COMPUTER READABLE FORM:
MEDIUM TYPE: IDPROPY STREN SO/10/103,686
FILING BATE: 25-MAT-2002
SOFTWARE: PATENTION COMPONEN
SOFTWARE: PATENTION NUMBER: US/10/103,686
FILING BATE: 25-MAT-2002
SOFTWARE: PATENTION NUMBER: 30,030
REGISTRATION AND STREN SO/10/103,686
FILING BATE: 20-MAT-1007
REDICATION NUMBER: 30,030
REDERRANCE CATANTON NUMBER: 30,030
REDERRANCE CATANTON NUMBER: 30,030
REDERRANCE CATANTON NUMBER: 30,030
TELECOMMUNICATION NUMBER: 30,030
REDERRANCE CHARACTERISTICS:
LENGTH: 433 BASE PATENTION:
TELECOMMUNICATION INFORMATION:
TERRATURE: TOPS.

MANDRESTER SOFTWARE: TOPS.

MANDRESTER
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity
Matches 370; Conserv
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STREET: 69
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LOCATION:
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TITLE OF INVENTION: "MONREX MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
CORRESPONDENCES: 12
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                ; Score 423; DB 7;
; Pred. No. 4.3e-97;
0; Mismatches 0;
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699 Prince Street
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07-JUN-1995
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GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
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LOCATION: 58..423
SEQUENCE DESCRIPTION: SEQ ID
                                                                                  Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 423; Conservative 0;
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MEDIUM TYPE: Floppy
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FILING DATE: 07-JUN-
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STREET: 699 Princ
CITY: Alexandria
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US-09-758-173-11
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Sequence 11, Application US/09526098

GENERAL INFORMATION:
APPLICANT: ANGERSON, DAITELL R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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Pred. No. 2.1e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                        012712-131
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                     35,030
                                                                                                                                                           LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                               TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.0%;
ilarity 84.5%;
Conservative
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1..1431
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APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: "DO HUMAN B7 1. AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"

CORRESPONDENCE: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STRRETS 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAACTGGTGGACCTGGATCCGCCAGCCC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/948,429B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 313.2; DB 5
Pred. No. 2.1e-69;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TRIREPHONE: 703-836-6620
                                                                                         RESULT 4
US-09-948-429B-11
Sequence 11, Application US/09948429B
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO: 11:
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84.5%;
 406 CTGGTCACCGTCTCTCA 423
                 421 CTGGTCACCGTCTCCTCA 438
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nucleic acid
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LENGTH: 1431 base pair
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Best Local Similarity 84.5
Matches 370; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: peptide
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LOCATION: 1..1
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US-09-948-429B-11
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                                                                                                                                             Patentin Release #1.0, Version #1.30
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Pred. No. 2.1e-69;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                         012712-131
                                                                                                                                                                                                                                                                                            US 08/487,550
                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFRERUCE/DOCKET NUMBER: 01271
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEPHONE: 703-836-620
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 74.0%;
Best Local Similarity 84.5%;
Matches 370; Conservative
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                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Alexandria
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LOCATION: 1..1
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                                                                                                                                                 SOFTWARE
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TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN
AND B7.2 CO-STIMULATORY ANTIGENS
                                                                                                                                                                                                                                              180
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                                                                                          Length 1431;
                                                                                                                           Indels
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ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. BOX 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                             53;
                                                                                            DB 5;
                                                                                      Score 313.2; DB 5
Pred. No. 2.1e-69;
0; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <a href="https://doi.org/10/10/10/14/">CLASSIFICATION DATA:</a>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
APPLICATION NUMBER: US 08/487,550
. LOCATION: 1..1431
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-971-631-11
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HANNA, Nabil
BRAMS, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-073-138-6; Sequence 6, Application US/10073138; GENERAL INFORMATION:
                                                                                            74.0%;
84.5%;
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                                                                                          Query Match 74.0
Best Local Similarity 84.5
Matches 370; Conservative
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US-09-971-631-11
Sequence 11, Application US/09971631
Sequence 11, Application US/09971631
GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS IMMUNOSUPPRESANTS"
                                                                                                                                                                          300
                                                                                                                                                                                                                                                              300
          TGCGCTGTCTCTGGTGGCTCCATCAGCGGTGGTTATGGCTGGGGCTGGATCCGCCAGCCC 180
                                                            181 CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC
                                                                                                           241 AACCCGTCCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/383,916
FILING DATE: 26-AUG-1999
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/971,631
FILING DATE: 09-0ct-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
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ADDRESSEE: BURNS, DOANE, STREET: 699 Prince Street
CITY: Alexandria
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TELEFAX: 703-836-2021
N FOR SEQ ID NO: 11:
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                                                                                                                                                                                                                                                                                                                                421 CTGGTCACCGTCTCCTCA 438
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1 ATGAAACACCTGTGGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,807
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                                                                                                                                                                                                                                                     FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/383,916
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1431 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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; LOCATION:
US-10-124-807-11
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TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN BY.1 AND/OR BY.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
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                                                                                                                                                                                                                                                                                                                                                                                                74.0%; Score 313.2; DB 6
84.5%; Pred. No. 2.1e-69;
iive 0; Mismatches 53
                               NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
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                                                                                                                                                                                                                                                                                                       LOCATION: 1..1431
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/10124807 GENERAL INFORMATION:
FILING DATE: 07-JUN-1995
                                                                                                                                                                            LENGTH: 1431 base pairs
                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                          INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                      linear
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Best Local Similarity 84.5
Matches 370; Conservative
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STREET: 69
CITY: Alex
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APPLICANT: Anderson, Darrell R.

APPLICANT: Anderson, Darrell R.

HITLE OF INVENTION: "MONKEX MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARNACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
TOWBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                                                                             CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTAC
                                                AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                                          361 GCCCAAATAGCTGGAACAA-------CGCTAGGCTTCTGGGGCCAGGGAGTC
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COMPUTER: IBM PC compatible
COMPUTER: EMP PC COMPATIBLE
COMPUTER: DATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/030,390
FILING DATE:
APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 09/383,916
FILING DATE:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-UN-1995
ATTORNEY,AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 01,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
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STREET: 699 Prince Street
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                  421 CTGGTCACCGTCTCCTCA 438
                                                                                                                                                                                                                                                                                                                                                                               406 CTGGTCACCGTCTCCTCA 423
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MOLECULE TYPE: peptide
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LOCATION: 1..1
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LOCATION:
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STATE: VA
COUNTRY:
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                                                                                                                     GENERAL INFORMATION:
APPLICANT: Anderson, Darrell R.
APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B1.2 PRIMATIZED FORMS THEREOF,
TITLE OF INVENTION: PHARMACEUTAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
TITLE OF INVENTION: IMMUNOSUPPRESANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
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MEDIOW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/124,905
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Pred. No. 2.1e-69;
0; Mismatches 53;
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APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1431 base pairs
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STRANDEDNESS: not relevant
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Best Local Similarity 84.5%;
Matches 370; Conservative
421 CTGGTCACCGTCTCCTCA 438
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LOCATION: 1..1
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; LOCATION:
US-10-124-905-11
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REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
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CORRESPONDENCE ADDRESS
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Best Local Similarity 83.59
Matches 353; Conservative
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                                                                                                1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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Sequence 7, Application US/10211357
GENERAL INFORMATION:
RAPLICANT: Hanna, Nabil
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
NUMBER OF SEQUENCES: 59
CORRESPONDENCES: 59
CORRESPONDENCES: BURNES, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
                                                                                                                         1 ATGAAACACCTGTGGTTCTTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG
                                                                                                                                                                                                                            AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
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                                                                      15;
                                            Length 1431;
                                                                    Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                         Score 313.2; DB 7;
Pred. No. 2.1e-69;
0; Mismatches 53;
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APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-Jul-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-Aug-2002
CLASSIFICATION: <Unknown>
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ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Teskin, Robin L
                                         Query Match
Best Local Similarity 84.5%;
Matches 370; Conservative
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US-10-030-390-11
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61 CIGCAGCIGCAGGAGICGGGCCCAGGAGIGGIGAAGCCIICGGAGACCCIGICCCICACC 120
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US-10-211-357-9
US-10-211-357-9
Sequence 9, Application US/10211357
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Newman, Roland A.
TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
Therapy
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83.5%; Pred. No. 4.9e-66;
iive '0; Mismatchės 67
35,030
3ER: 012712-165
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mat_peptide; LOCATION: 1.1404; SEQUENCE DESCRIPTION: SEQ ID NO: 7: US-10-211-357-7
                                           TELECOMMUNICATION INFORMATION
                                                                                                                                             LENGTH: 1404 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                               TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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358 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 417
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APPLICANT: Hanna, Nabil
Newman, Roland A.
Newman, Altchell E.
TILE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
                                                                       361 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCCAGGGAGTCCTGGTCACCGTCTCC
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CONDITER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

COMPARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/211,357

FILING DATE: 05-Aug-2002

CLASSIETCATION: CURNOWN>

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWECKER & MATHIS
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FILING DATE: 10-3u1-2000
APPLICATION NUMBER: US 08/523,894
FILING DATE: 06-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 31-165
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RADBRESSER: BURNS, DOANE, STREET: 699 Prince Street
CITY: Alexandria
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TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
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SEQUENCE CHARACTERISTICS:
LENGTH: 1404 base pairs
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STRANDEDNESS: single
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LOCATION:
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US-10-211-357-11
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                                                                                                                                                                                                             CURRENT APPLICATION DATA:

CURRENT APPLICATION NUMBER: US/10/211,357
FILING DATE: 05-4ug-2002
CLASSIFICATION NUMBER: US/10/211,357
FILING DATE: 05-4ug-2002
CLASSIFICATION NUMBER: US/09/612,914A
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 10-5-4ug-2000
APPLICATION NUMBER: US/09/612,914A
FILING DATE: 06-5pp-1995
ATTORNEY ABED 10 Spp-1995
ATTORNEY ABED 10 Spp-1995
ATTORNEY ABED 10 Spp-1995
ATTORNEY ABED 10 Spp-1995
ATTORNEY ABED 10 NOWBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-886-6620
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTER 5712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
      SWECKER & MATHIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.9%; Score 299.8; DB 6; 83.5%; Pred. No. 4.9e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                               COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : NAME/KEY: mat_peptide
; LOCATION: 1..1404
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-211-357-9
ADDRESSEE: BURNS, DOANE, STREET: 699 Prince Street CITY: Alexandria
                                                                                                     ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1404 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
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Matches 353; Conservative
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LOCATION:
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                                                                                                             SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NEWMAN, ROLAND A.
APPLICANT: HANNA, NABIL
APPLICANT: RAAB, RONALD W.
TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
FILE REFERENCE: 037003-0280614
CURRENT APPLICATION NUMBER: US/09/850,165
CURRENT FILING DATE: 2001-05-08
                                                                                                                                         PRIOR FILING DATE: 1991-07-25
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                PRIOR APPLICATION NUMBER: 07/856,281
PRIOR FILING DATE: 1992-03-23
PRIOR APPLICATION NUMBER: 07/735,064
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 07/912,292 PRIOR FILING DATE: 1992-07-10
                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 08/397,072 PRIOR FILING DATE: 1995-04-17
                                                                                                                                                                                                                                                                                                              PRIOR EILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/082,472 PRIOR FILING DATE: 1998-05-21
                                                                                                                              SOFTWARE: PatentIn Ver.
OTHER INFORMATION: Description OTHER INFORMATION: anti-CD4 VH
                                                   ORGANISM: Artificial Sequence
                                        FEATURE:
                                                                                           LENGTH: 423
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of Artificial nucleic acid
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US-10-089-128-37
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Best Local Similarity
                                                                                                                                              APPLICANT:
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APPLICANT:
CURRENT APPLICATION NUMBER: US/10/089,128
CURRENT ETLING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 60/156,294: 60/155,760:
60/156,625: 60/167,542: 60/167,522: 60/167,453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: INCYTE GENOMICS, APPLICANT: HODGSON, David
                                                                TITLE OF INVENTION: MOLECULES FOR DIAGNOSTICS FILE REFERENCE: PT-1066 PCT
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                                                                                                AMSHEY, Stefan FONG, Willy T.
                                                                                                                                                                               ROSEBERRY, Ann M. WRIGHT, Rachel J. CHEN, Wensheng
                                                                                                                                                                                                                                                                                             CHALUP, Michael S.
HILLMAN, Jennifer
                                                                                                                                 YAP, Pierre E. STOCKDREHER, Theresa
                                                                                                                                                                                                                                                                                                                               SHAH, Purvi
                                                                                                                                                                                                                                                                                                                                                                                                                              RUSSO, Frank D. SPIRO, Peter A.
                                                                                                                                                                                                                              GREENAWALT, Lila B.
PANZER, SCOTT R.
                                                                                                                                                                                                                                                                                                                                                          COHEN, Howard J.
                                                                                                                                                                                                                                                                                                                                                                               DUFOUR, Gerard E.
                                                                                                                                                                                                                                                                                                                                                                                                BRATCHER, Shawn R.
                                                                                                                                                                                                                                                                                 JONES, Anissa L.
                                                                                                                                                                                                                                                                                                                                              ROSEN, Bruce H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINCOLN, Stephen E
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                                                                                                                                                                                                                                                               Jimmy Y.
                                                                                                                                                                 Tommy F
                                                                                                                                                                                                                                                                                                 Jennifer L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                David M.
                                                                                                                                                                                                                                                                                                                                                                                                               Steve C
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83.2%;
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Pred. No. 1.
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 60/155,939; 60/156,565; 60/156,6 60/167,517;
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RESULT 15
US-10-211-357-1
Sequence 1, Application US/10211357;
GENERAL INFORMATION:
APPLICANT: Hanna, Nabil
Nauman. Roland A.
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 444248.7.dec
US-10-089-128-37
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Best Local S
Matches 359
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                                                                                                                                                                                      Newman, Roland A.
Reff, Mitchell E.
TITLE OF INVENTION: Recombinant
                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTCA 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAACCTGAACTCTGTGACCGCCGCGGGACACGCGCGTGTATTACTGTGCCA----GAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aacccgtccctcaagagtcgactcgccatatcagtagacacgtccaagagccagttgtcc
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STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
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84.3%;
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                                                                                                                                                                                        Anti-CD4 Antibodies
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SOFTWA..

APPLICATION NUMBER.

FILING DATE: 05-Aug-20v.

CLASSIFICATION: CUNKNOWN>

PRIOR APPLICATION UNMBER: US/09/612,914A

APPLICATION NUMBER: US 09/523,894

FILING DATE: 10-Jul-2000

APPLICATION NUMBER: US 08/523,894

FILING DATE: 06-SEP-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION UNMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-

TELEPHONE: 703-836-6520

TELEPHONE: 703-836-620

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 420 base pairs

TYPE: nucleic acid

STRANDEDMESS: single

TOPOLOGY: linear

"VPE: DNA (genomic')
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity Matches 349; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                      304
                                                                                                                                                                                                                                                            184
                        361
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
                                                                                                                                                           TGCAGTGTCTCTGGTGGCTCCATCAGCGGTGACTATTATTGGTTCTGGATCCGCCAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION IN GENOME:
                                                                      CTGAAACTGAGGTCTGTGACCGCCGCGGACACGGCCGTCTATTACTGTGCGAGTAAT---
                                                                                              CTGAACCTGAACTCTGTGACCGCCGCGGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG
                                                                                                                                                                                                                                                            CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGGCACCAATTAC
                                                                                                                                                                                                                                                                               CCAGGGAAGGGACTGGAGTGGACTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: mat_peptide LOCATION: 61..420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHROMOSOME/SEGMENT: light variable domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Monkey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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4..420
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83.1%;
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Pred. No. 6.5e-65;
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Length Indels

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63

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180

300 243 240 183

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of CE9

Db 361 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
Search completed: September 23, 2002, 19:58:47
Job time: 7177 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       2313.2
2399.8
2299.8
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2298.2
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1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

6: /cgn2_6/ptodata/1.
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Copyright (c) 1993 - 2000 Com
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*
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US-08-478-039-107
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209.8	210	213.2	217	217.6	221.2	223.6	227.2	236.6	237.8	237.8	237.8	237.8	238	238.2	239.6	241.4	243
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357	384	357	363	372	687	631	1418	622	366	366	366	366	800	650	1212	840	800
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Sequence 3, Appli	Sequence 49, Appl	Sequence 20, Appl	Sequence 50, Appl	46,	Sequence 34, Appl	Sequence 31, Appl	Sequence 7, Appli	Sequence 59, Appl	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 39, Appl	Sequence 4, Appli	Sequence 61, Appl	Sequence 4, Appli	Sequence 55, Appl

ALIGNMENTS

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; NAME/KEY:
; LOCATION:
US-08-803-085-2
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US-08-803-085-2
; Sequence 2, Application US/08803085
; Patent No. 6011138
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                                                                                                                                                                                                                                                                     TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: REFF, Mitchell E.
APPLICANT: REFF, Milliam S.
APPLICANT: KLOETZER, William S.
APPLICANT: NAKAMURA, Takehiko
APPLICANT: NAKAMURA, TAKEHIKO
APPLICANT: NAKAMURA, TANTI-HUMAN CD23 MONOCLONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,
                                                                                                                                                         FEATURE:
                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/0 FILING DATE: 20-FEB-1997 CLASSIFICATION: 424
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STREET: P.O. Box
CITY: Alexandria
                                                                                                       LOCATION:
                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                           STRANDEDNESS: single
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US-08-487-550-11

; Sequence 11, Application US/08487550

; Patent No. 6113898
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                TELEFAX: 703-836-2021 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 703-836-6620
                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  STREET: 699 princ
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241
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                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: OPENSYMS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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                                                                        NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                    CLASSIFICATION:
                                                                                                                                                APPLICATION NUMBER: US/08/487,550 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
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PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF
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Pred. No. 3.4e-114;
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US-08-487-550-11
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Best Local Sin
Matches 370;
                                                                                                                                                                                                                                                                  Sequence 7, Application US/08523894 Patent No. 6136310
                                                                                                                                          APPLICANT: Newman, Roland A. APPLICANT: Reff, Mitchell E. TITLE OF INVENTION: Recombinan TITLE OF INVENTION: Therapy NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                       GENERAL INFORMATION:
ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS.
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                                                                                                     STREET: 699 Prince CITY: Alexandria
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                                                                         COUNTRY:
                                                                                         STATE:
                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGTCACCGTCTCCTCA 438
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                                                                                                                                    SWECKER & MATHIS
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Pred. No. 4.5e-82;
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RESULT 4
US-08-523-894-9
; Sequence 9, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
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Best Local Similarity
Matches 353; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
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CLASSIFICATION:
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STRANDEDNESS: single
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| TCA 420
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milarity 83.5%;
Conservative
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Best Local S
Matches 353
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ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/08/523
FILING DATE: 06-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 0127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: FEATURE:
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ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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Local Similarity 83.5%;
nes 353; Conservative
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            AACCCGTCCCTCAAGAGTCGAGTCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
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Newman, Roland A.
Witchell E
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Pred. No. 3.5e
0; Mismatches
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nes 67;
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US-08-523-894-11
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Matches
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                                                 Query Match
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                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-620
TELEPAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                             FEATURE:
NAME/KEY:
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CURRENT APPLICATION DATA:
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ZIP: 22314-3187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Newman, Roland A.
APPLICANT: Reff, Mitchell E.
APPLICANT: Recombin
                                                                                                                       FEATURE:
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ORIGINAL SOURCE:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
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LOCATION:
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                                   Local
                                                                                                                                  LOCATION:
                                                                                                                                                                    CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                        NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/523,894 FILING DATE: 06-SEP-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                              CHROMOSOME/SEGMENT:
                                                                                                                                                                                                        ORGANISM:
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
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1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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SYSTEM: PC-DOS/MS-DOS
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                                   70.9%;
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                                                                                                                                                                   heavy chain gamma 4 with the P and mutation
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Pred.
                        Mismatches
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3.5e-78;
67;
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US-08-379-072A-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                    APPLICATION NUMBER: US 07/856,281 FILING DATE: 23-MAR-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 012712-067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                        APPLICATION NUMBER: US 0 FILING DATE: 25-JUL-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              FILING DATE: 10-JUL-: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 20
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STATE: Virginia
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                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/912,292
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P.O. Box 1404
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RAAB, Ronald W.
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                                                                            Teresa Stanek
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                                                                                                                                                                                                                                                                                                  patent No. 5693780
GENERAL INCOMMATION:
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                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                             TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                           APPLICANT: NEWMAN, Roland
APPLICANT: HANNA, Nabil
APPLICANT: RAAB, Ronald W.
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MOLECULE TYPE:
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LENGTH: 423 base pairs
                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                 CITY: Alexandria
STATE: Virginia
APPLICATION NUMBER: FILING DATE:
                                                                                                                                   COUNTRY:
                                                                                                                                                                                ADDRESSEE: Burns, Doane, STREET: P.O. Box 1404
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83.2%;
              US/08/481,869
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Pred. No. 6.8e-78;
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Best Local :
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19
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FILING DATE: 25-JUL-1991
ATTORNEY AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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LENGTH: 423 base pairs
TYPE: nucleic acid
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APPLICATION NUMBER: I
FILING DATE: 23-MAR--
PRIOR APPLICATION DATA:
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421
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APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
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Local Similarity 83.2%;
tes 352; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               64 GTGCAGCTGCAGGAGGCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
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TCA 423
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Pred. No. 6.8e-78;
0; Mismatches 68
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US-08-476-237-15

Sequence 15, Application US/08476237
Patent No. 5756096
GENERAL INFORMATION:
APPLICANT: NEWMAN, Roland A.
APPLICANT: HANNA, Nabil

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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: RECOMBINANT ANTIBODIES FOR HUMAN THERAPY
NUMBER OF SEQUENCES: 16
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361 ATATTGAAATATCTTCACTGGTTATTATACTGGGGCCAGGGAGTCCTGGTCACCGTCTCC
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REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: P.O. Box CITY: Alexandria
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 423 base pairs
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                                  GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                            CTGAACCTGAACTCTGTGACCGCCGCGGGCGGGCCGTGTATTACTGTGCCAGAGATTGG
                                                                                                                                                                        AACCCGTCCCTCAAGAGTCGAGCACCATTTCACAAGACACGTCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                    CCAGGGAAGGGACTGGAGTGGACGTATCTCTGGTAGTGGTGGGGCCCACCAACTAC 240
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                                                                        CTGAAACTGAGGTCTGTGACCGCCGCGGACACGGCCGTCTATTACTGTGCGAGTAAT---
                                                                                                                                                  AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC
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/: United States
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P.O. Box 1404
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Query Match Best Local Similarity

69.8%; 83.1%;

Score 295.2; DB 1; Pred. No. 5.1e-77;

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US-08-478-039-107
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Patent No.
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-11992
PRIOR APPLICATION UNMBER: US 07/856,281
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                 MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin
                                                                                                 FEATURE:
                                                                                                                                  POSITION IN GENOME
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CORRESPONDENCE ADDRESS:
                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111
421 TCA 423
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                                                                                                                                                                                                                                                                                                                                                   NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/379,072 FILING DATE: 25-JAN-1995
               NAME/KEY:
LOCATION:
                                                                LOCATION:
                                                                                 NAME/KEY:
                                                                                                                CHROMOSOME/SEGMENT:
                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                                                                                                                                                                                                                  LENGTH: 420 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107, Application US/08478039
o. 5681722
                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/08/478,039
07-JUN-1995
                                                                                                                                                                                                                   not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roland A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/735,064
                                                                                                                Anti-CD4
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ER: 012712-160
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US-08-476-349A-107
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APPLICANT: Hanna, Nabil
APPLICANT: Raab, Ronald W.
TITLE OF INVENTION: Recombi
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: DURNS, DOANE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 107, Application US/08476349A Patent No. 5750105
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                                                                                                                                                         APPLICATION NUMBER: US 07/
FILLING DATE: 10-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 23-MAR-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08
FILING DATE: 25-JAN-1995
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                      APPLICATION NUMBER: US 0
FILING DATE: 25-JUL-1991
ATTORNEY FACTOR TO THE PROPERTY INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Teskin Esq., Robin L. REGISTRATION NUMBER: 35,030 REFERENCE/DOCKET NUMBER: 01:
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/01 FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                 US 07/856,281
                                                                                                                                                                                                                                                                                                                                                                                   US 08/379,072
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012712-161
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US-08-523-894-1
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                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08523894 Patent No. 6136310
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Best Local Similarity 83.18;
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Hanna,
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                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                               APPLICANT: Newman, Roland A. APPLICANT: Reff, Mitchell E. TITLE OF INVENTION: Recombinant TITLE OF INVENTION: Therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                              NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

Version

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DMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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INFORMATION FOR SEQ ID NO: 1:
SEQUIENCE CHARACTERISTICS:
LENGTH: 420 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Matches 349
Sequence
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REGISTATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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Local Similarity 83.1%;
les 349; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/523,894 FILING DATE: 06-SEP-1995 CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                      CTGAAACTGAGGTCTGTGACCGCCGCGGCGGACACGGCCGTCTATTACTGTGCGAGTAAT---
                                                                                                                                                                                                       AACCCGTCCCTCAAGAGTCGAGTCATTCACAAGACACGTCCCAAGAACCAGTTCTCC
                                                                                                                                                                                                                                                                CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGGGGCCACCAACTAC
                                                                                                                                                                                                                                                                                                                              TGCGCTGTCTCTGGTGGCTCTGTCAGCAGTAGTAGTGGTGGACCTGGATCCGCCAGCCC
                                                                                                                                                                                                                                                                                                                                                                 GTGCAGCTGCAGGAGGCCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC
                                                                                                                                                                                                                                                                                                                                                                                CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTTCGGAGACCCTGTCCCTCACC 120
                                                                                                 GCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCC 420
                                                                                                                                                           CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG
                                                                                                                                                                                      AATCCCTCCCTCAACAATCGAGTCTCCATTTCAATAGACACGTCCAAGAACCTCTTCTCC
                                                                                                                                                                                                                                                CCAGGGAAGGGACTGGAGTGGATCGGCTACATCTATGGCAGTGGTGGGGGGCACCAATTAC
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3, Application US/08487550
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Pred. No. 5.1e-77;
0; Mismatches 68
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; LOCATION:
US-08-487-550-3
                                                                                                                                                                                                                                                                                                                                                                         Matches 357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6113898
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 703-836-2021
INFORMATION FOR SEQ.ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Anderson, I
TITLE OF INVENTION: TO
TITLE OF INVENTION: PI
TITLE OF INVENTION: PI
TITLE OF INVENTION: II
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                           61 CTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAAGCCTTCGGAGACCCTGTCCCTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                          1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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CTGAACCTGAACTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCCAGAGATTGG
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                                               CCAGGGAAGGGACTGGAGTGGATTGGACGTATCTCTGGTAGTGGTGGTGGGGCCACCAACTAC
                                                               AACCCGTCCCTCAAGAGTCGAGTCATCATTTCACAAGACACGTCCCAAGAACCAGTTCTCC
                                                                                                             CCAGGGAGGGGACTGGAGTGGATTGGCCATATTTATGGTAATGGTGCGACCACCAACTAC
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699 Prince
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81.5%;
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TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF
IMMUNOSUPPRESANTS"
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Pred. No. 5.1e-76;
""iematches 66;
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361 GCCCAAATAGCTGGAACAA-----

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                                                                                  Query Match
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                                                         Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
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APPLICANT:
APPLICANT:
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
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                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: PANCTU
CLONE: 1513264
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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CITY: Palo Alto
STATE: CA
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                      Local Similarity
                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                             LENGTH:
                            1 ATGAAACACCTGTGGTTCTTCCTCCTCCTGGTGGCAGCTCCCAGATGGGTCCTGTCCCAG 60
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INFORMATION:
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                                                                                                                                                                                                                              1567 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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Corley, Neil C.
Guegler, Karl J.
                                                                                                                                                         PANCTUT01
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Yue, Henry
                                                        Conservative
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                                                                   Score 289.6;
Pred. No. 3.4
                                                        Mismatches
                                                                     3.4e-75;
                                                                                  DB 3;
                                                                                 Length 1567;
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Patent No. 5
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
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TITLE OF INVENTION: REACTIVE NI
TITLE OF INVENTION: ANTI-9p 12:
TITLE OF INVENTION: AND USE TH
                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 617-523-3400
                                                                                                                                       FILING DATE: 10-DEC-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                             TELEX:
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                    ZIP:
                                                                                                                                                                        APPLICATION NUMBER: 08/400,674 FILING DATE: 08-MAR-1995 APPLICATION NUMBER: 07/804,652
                                              TELEFAX:
                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                     FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                      COMPUTER:
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                                                                                                                          Resnick, David
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CURRENT APPLICATION DATA:

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US-09-042-353-357; Sequence 357, Application US/09042353; Patent No. 6255458
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; NAME/KEY: mat_peptide;
; LOCATION: 58...426
; OTHER INFORMATION:
US-08-480-774A-1
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                                                                                                                                                                                                                                     Patent No. 6255458
GENERAL INFORMATION:
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Best Local
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                   APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
FEATURE:
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CITY: San Francisco
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nucleic acid
DEDNESS: single
OGY: linear
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Two Embarcadero
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Pred. No. 4
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No. 4.2e-69;
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; TOPOLOGY: 1; MOLECULE TYPE: US-09-042-353-357
                                                                                                                                   TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                 REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER. US 08/096,762
APPLICATION NUMBER.
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 403 base pairs
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FILING DATE: 10-DEC-
PRIOR APPLICATION DATA:
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                                                      TYPE: nucleion STRANDEDNESS:
                                                                                                                                                                                                                             NAME: Apple, Randolph REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/352,322 FILING DATE: 07-DEC-1994
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                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/758,417 FILING DATE: 02-DEC-1996
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                                                                nucleic acid
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10-OCT-1995
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10-DEC-1993
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23-JUN-1992
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Query Match
Best Local Similarity

62.9%;

Score 266.2; Pred. No. 1.4 Mismatches

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403; 21;

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Search completed: September 23, 2002, 18:00:51 Job time: 3222 sec

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Listing first 45 summaries
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Perfect score:
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                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Score
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length: 2000000000
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Match Length
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115:::
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Copyright (c) 1993 - 2000 Compugen
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AUTHORS

MOTOR_J.S., Nowell, P.C., Roelcke, D., Pruzanski, W., Roudler, J. and Silverman, G. J.

Variable region (IGL@)

M74019.1 GI:186042

KEYWORDS
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                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 729)
Serizawa, N., Haruyama, H., Nakahara, K. and Tamaki, I. Humanized anti-Fas antibody
Patent: JP 2000166574-A 85 20-JUN-2000;
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Humanized anti-Fas antibody.
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/map="22q11.1-q11
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Andris,J.S., Miller,A.B.,
and Capra,J.D.
Variable Region Gene Segment Utilization in Rhesus Monkey Hybridomas Producing Human Red Blood Cell-Specific Antibodies: Predominance of the VH4 Family but not VH4-21 (V4-34) Unpublished
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Macaca mulatta Ig rearranged
antibody, mRNA, partial cds.
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C12N15/09,A61K39/00,A61K39/395,A61K39/395,A61P37/02,A61P43/00,
C07K16/18,
C12N1/21,C12N5/10,C12P21/08//(C12N1/21,C12R1:19),C12N15/00, PC
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                                                                                        monoclonal antibody C: E12918 E12918.1 GI:3251749 JP 1997100300-A/2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Co
University of Texas Southwestern Medical Center, 6000 Harry
Blvd., Dallas, TX 75235-9140, USA
                                                                                                                         E12918 396 bp DNA Human mRNA for variable region of light monoclonal antibody CLN''l-IgM, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to Andris, J.S., Mi
Hagiwara,H., AOZUKA,Y. and Miyahara,J
AMINO ACID SEQUENCE OF ANTICANCER HUMBASE SEQUENCE CODING FOR THE SAME
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                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 396)
                                                                 Homo sapiens
                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDMRALTQLLGLLLLWLPGARCDIQMTQSPSSLSASVGDRVTIT CRASQGISDYVNWYQQKPGKAPKRLIYAASSLESGVPSRFSGSGSGTEFTLTISSLQP EDFATYYCLQYNSDPFTFGPGTKLDIKR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="immunoglobulin light chain"
/protein_id="AAB09448.1"
/db_xref="GI:1575090"
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/note="hybridoma 1D8"
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Miller,A.B.,
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91.5%;
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                                           Craniata; Vertebrata; Catarrhini; Hominidae.
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+~hes 33;
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           MONOCLONAL ANTIBODY
                                             Hominidae;
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                                            Euteleostomi; Homo.
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                                           CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCCTCGGACGTTC
                                                                                                                                                                                              GTCACCATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAG
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GGCCAAGGGACCAAGGTGGAAATCAAA
                              CAACCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCAGACGTTC
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CC strandec
CC topology
FH Key
FT source
FT sig_pept
FT sig_pept
FT mat_pept
FT misc_feature
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PN JP 1997100300-A/2

PD 15-ABR-1997

PF 03-OCT-1995 JP 1995278266

PI HAGIWARA HIDEAKI, AOZUKA YASUYUKI, MIYAHARA JUNICHI PC
C07K16/42,C07H21/04,C12N15/02,C12N15/09//A61K39/395,C12N5/10,
C12P21/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent: JP 1997100
HAGIWARA YOSHIHIDE
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    region (CDR3)'.
Location/Qualifiers
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/db_xref="taxon:9606"
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91.5%;
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/cell_type='hybridoma ce
/cell_line='HT-2'
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/note='this region
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Pred. No. 1.1e-98;
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 406)

Aucouturier,P., Bauwens,M., Khamlichi,A.A., Denoroy,L., Spinelli,S., Touchard,G., Preud'homme,J.L. and Cogne,M.

Monoclonal Ig L chain and L chain v domain fragment crystallization in myeloma-associated Fanconi's syndrome J. Immunol. 150 (8 Pt 1), 3561-3568 (1993)
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Human rearranged IgK mRNA VJC
MR7479
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immunoglobulin light chain.
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                                                                                                                                                                                                                                                                                                                                 /note="VI-J1 region" 389. .>406
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CRASQTIATFLNWYQQKPGKAPKLLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQP
EDFATYYCQQSYSIPWTFGQGTKVEIKRTVAAP"
                                                                                                                                                                                                                                    /gene-"IgK"
/note-"This CDS feature is included to show the
/note-"This CDS feature is included to show the
translation of the corresponding C_region. Presently
translation qualifiers on C_region features are ille
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/product="immunoglobulin kappa-chain VK-1"
/prottein_id="AAA51019.1"
/db_xref="GI:185951"
                                                                                                                                                                /translation="RTVAAP"
113 c 102 g
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/db_xref="GI:561655"
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/isolate="patient CHEB"
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/product="immunoglobulin
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91.2%;
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                                                                                         Score 332.6;
Pred. No. 3.8
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                                                                                                       DB 9;
                                                                                                     Length 406;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maloum,K., Dighiero,G. and Magnac,C.C. Unmutated Ig VH genes in CLL patients Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 400)
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (13-JAN-2000) Physiopathology, du DR Roux, Paris 75015, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 400)
Maloum,K., Dighlero,G. and Magnac,C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene, partial cds.
AF228327
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Homo sapiens clone BUS immunoglobulin light chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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     99
/translation="DMRVPAQLLGLLLLWLRGARCDIQMTQSPSSLSASVGDRVTITC RASQSISNYLNWYQQKPGKGPKLLIHAASSLQSGVPSRFSGSGSGTDFTLTISSLQPE DFATYYCQQSYSTPRTFGQGTKVEIKRIRAR" 109 c 100 g 92 t
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                                                                                                                                                                                     /product-"immunoglobulin light
                                                                                                                                                                                                                             patient"
                                                                                                                                                                                                                                              /rearranged
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                                                                                                                                                                                                                                                                                     /map="14q32-q39"
/clone="BUS"
                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                      /note="unmutated"
                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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85.6%; 91.4%;

Score Pred.

331.2; DB 9; No. 1.1e-97;

Length

1;

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KEYWORDS
SOURCE
ORGANISM
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGGACTTTTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTC
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L01279
                                                                                                                                                                                                                                                                                                                                                Nowell,P.C. and Silberstein,L.E. Variable region gene analysis of an isotype-switched (IgA) variant of chronic lymphocytic leukemia Blood 80 (9), 2287-2297 (1992) 93043344
                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 432)
Friedman, D.F., Moore, J.S., Erikson, J., Manz, J., Gold
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                          /Codon_start=1
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                                                                                                                                                                                                                           /map="2"
                                                                                                                                                                                                                                            /map="2p12"
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/isolate="CLL-412"
                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                                                                                                                                                          db_xref="taxon:9606"
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Best Local Similarity
                                                             JOURNAL
                                                                           TITLE
                                                                                                       AUTHORS
                                                                                                                                                                                TITLE
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                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta Ig rearranged light chain variable antibody, mRNA, partial cds.
                                                                                                                                                                                        I (bases 1 to 390)
Andris, J.S., Miller, A.B.,
and Capra, J.D.
                             Submitted (06-MAY-1996) J.S. Andris, Molecular Immunology Center, University of Texas Southwestern Medical Center, 6000 Harry Hines Blvd., Dallas, TX 75235-9140, USA
                                                                           Direct Submission
                                                                                       and Capra, J.D.
                                                                                                    2 (bases 1 to 390)
Andris, J.S., Miller
                                                                                                                          Unpublished
2 (bases 1
                                                                                                                                                 Variable Region Gene Segment Utilization in Rhesus Monkey Hybridomas Producing Human Red Blood Cell-Specific Antibodies: Predominance of the VH4 Family but not VH4-21 (V4-34)
                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                        Macaca mulatta
                                                                                                                                                                                                                                                                                                                                   U57579.1
                                                                                                                                                                                                                                            Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                    rhesus monkey.
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/note="G00-119-341"
/gene="IGK"
/gene="IGK"
                                                                                                                                                                                                                                                                                                                                   GI:1575105
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126 c 102 g
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67. .354
              Location/Qualifiers
                                                                                                     Miller, A.B.,
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92.3%;
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Pred. No. 1.5e-97;
0; Mismatches 27;
                                                                                                       Abraham, S.
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                                                                                                     .R.,
                                                                                                    Cunningham, S.,
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                                                                                                       Blancher, A.
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                                                                                              Takashi,T., Katsunari,T.P. and Nobuaki,H.
Human monoclonal antibody against a costimulatory signal
transduction molecule ailim and pharmaceutical use there
Patent: EP 1158004-A 29 28-NOV-2001;
Japan Tobacco Inc. (JP)
                                                                                                                                                                                                                                            AX305000
Sequence 29 from Patent
AX305000
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                Homo sapiens
Eukaryota; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MDMRAPAQLLGLLLLWLPGARCDIQMTQSPSSLSASVGDRVTFT CRASENVNNXLHWYQQKPGKAPKLLIYGASTLQSGVPSRFSGSGSGTDFTLTISSLQP EDVATYYCQHSYGTPLTFGGGTKVEIKR"
                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="immunoglobulin light chain"
/protein_id="AAB09456.1"
/db_xref="GI:1575106"
/note="unnamed
/codon_start=1
                         39. .749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Macaca mulatta"
/db_xref="taxon:9544"
/note="hybridoma 1G7"
                                                                                 Location/Qualifiers
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90.78;
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Pred. No. 4.3e-97;
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Best Local
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CDS
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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                               AX306529
Sequence
AX306529
                                                                                                                                                                                    Human monoclonal antibody against a costimulatory signal transduction molecule ailim and pharmaceutical use there patent: WO 0187981-A 29 22-NOV-2001;
                                                                                                                                                                                                                                          Tsuji,T., Tezuka,K. and Hori,N.
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CRASQGISRLLAMYQOXPGKAPKLLIYVASSLQSGVPSRFSGSGSGTDFTLTISSLQP
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EYPREAKYQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
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39. 104
750. 2974
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/codon_start=1
                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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from Patent WO0187981.
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90.7%;
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Pred. No. 4.5e-97;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                          GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                                          CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
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                                                                          2 (bases 1 to 370)
2 (bases 1 to 370)
Klein,R., Jaenichen,R. and Zachau,H.G.
Expressed human immunoglobulin kappa genes
Eur. J. Immunol. 23 (12), 3248-3262 (1993)
                                                                                                                                                       Zachau, H.G.
Direct Submission
Submitted (26-APR-1993)
                                                                                                                                                                                                                                                                                           H.sapiens (I.131).
                                                                                                                                              Chemie,
                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 370)
                                                                                                                                                                                                                                                                              X72441
                                                                                                                                   FRG
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                  HSIGKLV20
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39.104
750.974
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/db_xref="taxon:9606"
/chromosome="2"
                           /organism="Homo sapiens"
/isolate="M.L."
                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                   GI:441350
                                                                                                                                                                                                                                                                                                      mRNA
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90.7%;
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                                                                                                                                                         H.G.
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r 44,
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                                                                                                                                                                                                                                 RESULT
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Best Local S
Matches 344
                                                                                                                  ORGANISM
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J_segment
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                                  Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 396)
Bensimon,C., Chastagner,P. and Z.
Low rate of receptor-editing in
Unpublished
                                                                                                                                                                               H.sapiens
Z27173
           Zouali,M.
                                                                                                                 Homo sapiens
                                                                                                                                          variable region.
                                                                                                                                                 z27173.1 GI:415961 immunoglobulin; imm
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/tissue_type="spleen"
/clone_lib="lambda zap
1. .370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=2
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/protein_id="CaA51109.1"
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/ISSYLNMYQOKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATY
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103 c
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93.08;
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                                                                                       Craniata; V
Catarrhini;
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                                                                                       Vertebrata;
i; Hominidae;
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                                                     anti-DNA
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                                                                                       Euteleostomi;
Homo.
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                                                                                                                                    GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                                                                                             CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                  AAACCAGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCACTTTGCAAAGTGGGGTC
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                                                                                                                                                                                                                                                                                                                                            AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                         ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                     349;
                                H.sapiens
(I.23).
X72477
          χ72477.1
C-region;
                                                                   HSIGKLV56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kappa gene rearrangements
EMBO J. 13 (13), 2951-2962 (1994)
94313975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bensimon, C., Chastagner, P. and Zouali, M. Human lupus anti-DNA autoantibodies unde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (03-NOV-1993) M. Zouali, Institut Pasteur, Immunogenetique Cellulaire, 28 Rue du Dr. Roux, 75015 Paris, 3 (bases 1 to 396)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   358. .396
/note="JK1"
a 112 c
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//codon_start=1
//product="IG light chain variable region (VJ)"
//protein_id="CAA81697.1"
//db_xref="GI:415962"
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ITCRASQGISSYLAWYOKPGKAPKLLIYAASTLQSGVPSRFSGSGSGTDFTLTISCL
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                                                        mRNA
                      GI:441422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="T21-9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="VK1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
          immunoglobulin;
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                                                     383 b
r rearranged
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Pred. No. 4.8e-96;
D; Mismatches 38
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         J-segment; kappa
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                                                  bp qd
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                                                    mRNA li
kappa light
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ht chain
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GTGGAAATCAAA 387
                                                          GCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGGGACCAAG
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                                            GGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTT
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Klein,R., Jaenichen,R. and Zachau,H.G.
Expressed human immunoglobulin kappa gr
Eur. J. Immunol. 23 (12), 3248-3262 (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (26-APR-1993) H.G. Zachau, Institut : Chemie, der Universitaet Muenchen, Schillerstr
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Submitted (26-APR-1993) H.
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Mammalia; Eutheria;
1 (bases 1 to 383)
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SISNYLMWYQRKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFAT
YYCQQSYNTPWTFGQGTKVEIKRTVA"
52. .336
337. .375
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376. .383
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/product="Ig kappa light chain (VJC)"
/protein_id="0AA51145.1"
/db_xref="GI:441423"
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/db_xref="taxon:9606"
/chromosome="2"
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/clone_lib="lambda za|
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/isolate="M.L."
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Pred. No. 7.6e-96;
""smatches 29;
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Best Local S
Matches 347
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                              AACCAGGGAAAGCCCCTAAGTTTCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGGTCC
                                              AACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCC
                                                                                    TCACCATCACTTGCCGGGCAAGTCAGAGCATTGGCACCTATTTAAATTGGTATCAGCAGA 180
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347; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (26-APR-1993) H.G. Zachau, Institut fuer Physiologische Chemie, der Universitaet Muenchen, Schillerstr 44, 8000 Muenchen
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X72427
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Direct Submission
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/product="19 kappa light chain (VJ)"
/protein_id="CAAS1095.1"
/protein_id="CAAS1095.1"
/db_xref="G1:441323"
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RASQSIGTYLNWYQQKPGKAPKFLIYGASSLQSGVPSRFSGSGSGTDFTLTISSLQPE
DPATYYCQQTYSTPPTFGGGTKVEIKL"
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/clone_lib="lambda zar
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/isolate="M.L."
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/chromosome="2"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Search completed: September Job time: 6866 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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BG541198
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BG557031 60256115
BG754732 602714301
BG754818 60271248
BG5548281 602572248
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AW388563 PM4-HT034
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BG7501164 602733253
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ALIGNMENTS

	FEATURES source		AUTHORS TITLE JOURNAL COMMENT	VERSION KEYWORDS SOURCE ORGANISM	RESULT 1 AW405753 LOCUS DEFINITION ACCESSION
/organism='Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:3057290" /clone=lib="NIH_MGC_37" /tissue_type="1ymph" /cell_type="germinal center B cells" /cell_line="MGC85" /lab_host="DH10B (LTI)" /note="Vector: pT/T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis	, , , , , , , , , , , , , , , , , , ,	Email: cgapbs-r@mail.nih.gov Eco RI site shown at the beginning of the sequence. Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: M.B. Soares Lab CDNA Library Arrayed by: M.B. Soares Lab DNA Sequencing by: M.B. Soares Lab Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html Seq primer: Mi3 Forward.	I (Mases I to 493) NIH-MGC http://mgc.nci.nih.gov/. NATIONAL Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D.	AW405753.1 GI:6924810 EST. human. human Sapiens Homo Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.	AW405753 493 bp mRNA linear EST 16-FEB-2000 UI-HF-BLO-abp-a-02-0-UI.rl NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3057290 5', mRNA sequence. AW405753

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AUTHORS
TITLE
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                                                                                                                              Unpublished (199)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.linl.gov
                                                                                                                                                                                                                                                                              1 (bases 1 to 891)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian
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                                                                                       Location/Qualifiers
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONFECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln1.gov
Plate: LLCM1506 row: m column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                    BG537031 /24 pp "602565115F1 NIH_MGC_77 Homo sapiens
                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 724)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 867)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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                                  mRNA sequence.
BG756818
BG756818.1 GI:
                                                                                        BG756818 886 bp mRNA linear EST 15-MZ 602710291F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4850686
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/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; CDNA made by Oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
25 a 245 c 215 g 182 t
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/clone="IMAGE:4854409"
/clone_lib="NIH_MGC_48"
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Plate: L/LM1692 row: e column: 23
High quality sequence stop: 864.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Cgapbs-r@mail.nih.gov

Email: Cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 886)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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Clone distribution: MGC clone distribution information can
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/lab_host="DH10B (phage-resistant)"
/note="Ovgan: B-cells; Vector: poTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:4850686"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Tissue Procurement: CLONTECH Laboratories, Inc
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/Clone_lib="NIH_MGC_77"
/Iab_Most="DH10B (TI phage-resistant)"
/Iab_Most="DH10B (TI phage-resistant)"
/Inote="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/Inote=
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AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
                                                       GGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCCATCA 246
                                                                                                          ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTTGGTATCAGCAGAAATCA 184
                                                                                                                             ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAGAAACCA 186
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                                  GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MCC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 391)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             98
                                                                                                                                                                                                                                                                                                                                                                                                                                         Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Low M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

a 108 c 94 g 91 t
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/cell_line="MGC85"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="NIH_MGC_37"
/tissue_type="lymph"
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/db_xref="taxon:9606"
/clone="IMAGE:3058060"
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91.18;
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                                  GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTAAATTTGGTATCAGCAG 180
                                                                                   AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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GTTACCATCACTTGCCGGCCAAGTCAGAGCATTAGTAGGTATTTAAATTGGTATCAGCAG
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                                                                                                                                                                                                             349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=PM4&t2=PM4-HT0348-
261199-001-A07&t3=1999-11-26&t4=1)
Seq.primer: puc 18 forward
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 bp mRNA linear
PM4-HT0348-261199-001-A07 HT0348 Homo sapiens cDNA,
AW383563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The FAPESP/LICR Human Cancer Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
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3P http://www.ludwig.org.br/ORESTES.
                                                                                                                                                                                                                                                                                                                   108
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                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                             /note-*Organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="HT0348"
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                                                                                              ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
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                                                              ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCCTCCTGCTACTCTGGCTCCGAGGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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IMAGE:3057288 5', mRNA sequence.
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/note="Vector: pT773-9c; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT773-9c; Site_1: Not1; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT773-9c; Site_1: Not1; Sit
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/clone_lib="NIH_MGC_37"
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/cell_type="germinal center B cells"
/cell_line="MGC85"
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Tissue Procurement: CLONTECH Laboratories,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (Clontes); Site_1:
/note="Organ: lung; Vector: pDNR-LIB (Clontes); Site_1:
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                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM1633 row: i column: 02
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BG685444
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National Institutes of Health, Mammalian
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602637305F1 NIH_MGC_48 Homo sapiens
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/Clone=lib="NIH_MGC_48"
/Clone=lib="NIH_MGC_48"
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/Lib_host="DH10B (phage-resistant)"
/Lib_host="DH10B (phage-resistant)"
/Lib_host="OH10B (phage-res
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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602245105Fl NIH_MGC_48 Homo sapiens
                                                                                                                                                                            cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC Clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 943)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BF976230
                                                                                                                                         http://image.llnl.gov
Plate: LLCM1208 row:
                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt,
                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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a 229 c 185 g 158 t 1 others
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4336225"
/clone_lib="NIH_MGC_48"
                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:12343445
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Pred. No. 3.1e-87;
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http://image.llnl.gov
                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF663472
602144635F1 NIH_MGC_48
                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                National Institutes of Health, Mammalian Unpublished (1999)
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NIH-MGC http://mgc.nci.nih.gov/.
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                  DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                     Tissue Procurement: Louis M. Staudt, M.D., Ph.D. CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (DNA Commentation by Transe Constitution of the Const
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/lab_host="pH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: ECORI; CDNA made by Oligo-dT priming.
Directionally cloned into ECORI/XhoI sites using the following 5' adaptor: GGCACGAGG). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 712)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999
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/lab_host="DH1DB (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI;XhoI sites using the
following 5' adaptor: GGCAGGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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Pred. No. 3.7e-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATCAAGGTTCAGCGGCAGTGGATCTGGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
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mRNA sequence.
BG341239
BG341239.1 GI:13147677
EST.
human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                          602463904F1 NIH_MGC_48
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/clone_lib="NIH_MGC_77"
/lab_most="DH10B (Tl phage-resistant)"
/lab_most=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cgapbs-r@mail.nih.gov
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/db_xref="taxon:9606"
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Pred. No. 5.3e-87;
0; Mismatches 34
                                                                                                                                                          Homo sapiens cDNA clone IMAGE: 4576560
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CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                                                                                      CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC 360
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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/lab_bost="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAGG9. Size-selected >500bp for average insert size 1.8kb. Library constructed by Lit Hong in the laboratory of German approximation of the construction of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NH_MGC Library."

247 c 229 g 191 t 1 others
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/clone="IMAGE:4576560"
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Search completed: September 23, 2002, 17:06:57 Job time: 4516 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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   342.2
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5: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1985.DAT: *
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secret	3135	22	930	5	92
Nucleotide sequenc	933	7.2	390	5	. 6
immune	H2679	22	928	75.8	293.2
Nucleotide sequenc	AAZ39322	21	372	6.	ĸ.
Monoclonal antibod	AAT85844	18	384	6.	
oclonal	AAT46133	17	384	6.	296.2
Sequence encoding	AAQ43773	14	702	ა	
DNA encoding nove	AAS76095	23	363	9	
Immunoglobulin rB6	AAT79921	18	366	6	297
Anti-interleukin-	AAQ87237	16	390	σ,	297.4
Nucleotide sequenc	AAZ39339	21	384	7.	97
Nucleotide sequenc	AAZ22020	20	3819	8	302
Plasmid pLC6G5 nuc	AAV39266	19	3819	8	302
Kappa light chain	AAT78825	18	3819	8	302
ന	AAZ22047	20	420	8	302
Synthetic kappa li	AAV39293	. 19	420	8	302
Human immunoglobul	AAT73445	18	420	8	302
tide	AAZ39326	21	372	8	2
Human IGFAM-13 imm	AAA27393	21	928	8	63
	AAT16181	17	389	æ	2
Humanized 1308F VL	AAQ67194	۲ 5	389	œ	60
Human anti-RSV mon	AAT61240	18	705	œ	304.2
Partial nucleotide	AAZ21995	20	439	8	20
Nucleotide sequenc	AAZ39325	21	387	9	306
nog lobu	AAT73443	18	439	9.	307
Functional kappa t	AAV39241	19	409	9.	307
93KA9 anti-Varicel	AAQ82749	16	387	9.	307
Nucleotide sequen	AAZ39320	21	384	.0	90
breast c	AAF44892	22	944	0	311.8
IGFAM-1 i	AAA27381	21	917	μ.	16
anti-HBs	AAQ49943	14	1066		16
IGFAM-9 i		21	817	<u>, </u>	16
Human IGFAM-10 imm	N 3	21	936	2	318
al nucleotid		20	388	82.2	18
Functional Kappa t	392	19	388	2	318.2
Human immunoglobul	AAT73441	18	388	۲,	18.

ALIGNMENTS

RESULT AAV33309

AAV33309 standard; DNA; 387 BP.

AAV33309;

18-NOV-1998 (first entry)

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Anti-human CD23 5E8 monoclonal antibody; light chain variable region; human CD23; IgE; FceRii/CD23; gamma-1 constant region; holiamation; autoimmune disease; allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
               misc_feature
                                                                                                                                         Key
                                             misc_feature
                                                                mat_peptide
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                                                                                                                                                                                                                                             Anti-human CD23 5E8 monoclonal antibody light chain variable region DNA
                                                                                                                                                                       Macaca fascicularis
/*tag= d
/note= "encodes CDR 1 region"
214..234
/*tag= e
                                             /*tag= c
136..168
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67..387
                                                                                                                                                 Location/Qualifiers
                                                                                               /note= "CDS does not contain a stop codon"
                                                                                                                    /product= "anti-human CD23 5E8 light chain variable
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AAZ39340

Nucleotide

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Best Local
                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a DNA sequence encoding the light chain variable region of primate monoclonal antibody anti-human CD23 5E8. The invention provides primate monoclonal antibodies which specifically bind human CD23, the low affinity receptor for IgE (FceRii/CD23), and comprise either of a human gamma-1 or human gamma-3 constant region that binds to human Fc gamma receptors and inhibits IgE expression. The monoclonal antibodies of the invention are claimed to be useful for inhibiting induced IgE production for treating or preventing allergic, inflammatory and autoimmune conditions e.g. allergic rhinitis conjunctivitis, autoimmune haemolytic anaemia, etc.
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            auto:immune
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20-FEB-1997;
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                                    CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                           GGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                                                                                              aaaccaggaaaagctcctaagctcctgatctatgttgcatccagtttgcaaagtggggtc
                                                                                                                               AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                     agatgtgacatccagatgacccagtctccatcttccctgtctgcatctgtaggggacaga
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                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 8.5e-109;
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gous recombination; vector; neomyc;
ne; selectable marker; immunoglobul
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Rhesus macaque polyoma
Photinus sp.
Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baculovirus
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specification. It is included to
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requences, in a pBR-derived backbone, and also an anti-human CD23 IgE receptor human gamma-1 monoclonal antibody 5E8 gene. The invention provides a novel method for integrating a desired exogneous DNA at a target site within the genome of a mammalian cell via homologous recombination. This involves transfecting the cell with a 'marker plasmid' such as Desmond (see AAV61702) ......
                                                   addition, the number or colors is reduced. An amplication of the marking vector, beinserted on integration of the marking vector, area is targeted to this site, the gene is further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell with a 'marker plasmid' such as Desmond (see AAV61792), which contains a unique sequence that is foreign to the mammalian cell genome and which provides a substrate for homologous recombination, followed by transfection with a 'target plasmid', such as Mandy or Molly (see AAV61793), containing a sequence which provides for homologous recombination with the unique sequences contained in the marker plasmid, and further comprising a desired DNA that is to be integrated into the mammalian collaboration of the marker plasmid, and further comprising a desired DNA that is
                                                                                                                                                                                             of a functional neo protein. The method is applicable to all mammalian cells, and can be used to express any type of recombinan protein. The use of a triply spliced selectable marker means that
                                                                                                                                                                                                                                                                                              targeting plasmid, and are separated by an intron into which at least one gene of interest is cloned. Homologous recombination of the targeting vector with the integrated marking vector results
                                                                                                                                                                                                                                                                                                                                                                   dominant selectable marker The neo gene is split into 3 exons Exon 3 is present on the marker plasmid and becomes integrated into the host cell genome upon integration of the marker plasminto the mammalian cells. Exons 1 and 2 are present on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               baculovirus DNA, a cassette comprising the promoter and enhancer elements from cytomegalovirus and Sy400 virus, the E. coli beta-glucuronidase (GUS) gene, firefly luciferase gene, an inactivated Salmonella typhimurium histidinol dehydrogenase (HisD)
                                                                                                                                                                        protein. The use of a triply spliced selectable marker meall selected colonies arise from homologous recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                           immunoglobulin or other secreted mammalian glycoprotein. The homologous recombination system utilises the neo gene as a dominant selectable marker. The neo gene is split into 3 exons.
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                                                amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to be integrated into the mammalian cells, typically an
                                                                                                                                                                                                                                                                     in correct splicing of all 3 exons of the neo gene and expression
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Sequence 19035 BP; 4705 A; 4968 C; 4822 ç; 4519 7, 21 other;

Ş, 밁 QY QΥ 밁 В В Ω Matches Best Query Match 7541 7601 7661 241 181 121 61 Local ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG aaaccaggaaaagctcctaagctcctgatctatgttgcatccagtttgcaaagtggggtc gtcaccatcacttgcagggcaagtcaggacattaggtattatttaaattggtatcagcag GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG agatgtgacatccagatgacccagtctccatcttccctgtctgcatctgtaggggacaga AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA atggacatgagggtccccgctcagctcctggggctccttctgctctggctcccaggtgcc AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGGTC 387; Similarity Conservative 100.0%; 0; Score 387; DB 19; Pred. No. 3.9e-108; Mismatches 0; Indels Length 19035; 0; Gaps 7720 7660 120 7600 60 180 240 300 0

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This invention describes a novel humanized anti-Fas antibody-like molecule (I) that, induces apoptosis in cells with an abnormal Fas/Fas ilgand system, by binding to Fas on the cell surface, and prevents apoptosis in cells with a normal system, by inhibiting binding between Fas and its ligand. The products of the invention have anti-inflammatory, anti-anemic, antidiabetic, anti-allergic, anti-arthritic, antiviral, immunomodulatory, dermatological, immunosuppressive, thyromimetic, anti-rheumatic, nephrotropic, anti-infertility, neuroprotective, antiarteriosclerotic, cardiant and hepatropic activity. (I) induce apoptosis by binding to cell surface Fas or inhibit it by competitive inhibition of ligand binding. (I) are used to treat and/or prevent diseases associated with the Fas/Fas ligand system, especially systemic versus host disease, Slorgen's syndrome, pernicious or hypoplastic anemia, Addison's disease, scleroderma, Goodpasture syndrome, Crohn's disease, autoimmune hemolytic anemia, sterility, myasthenia gravis, multiple sclerosis, Basedow's disease, thrombopenia purpura, insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic; hepatotropic; humanized; apoptosis; systemic lupus erythematosus; Hashimoto disease; rheumatoid arthritis; graft versus host disease; Sjorgen's syndrome; anemia; Addison's disease; scleroderma; sterility; Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis; multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy; insulin dependent diabetes mellitus; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection; ss.
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                                                                                                                                                                                                                                                                                                                                                                         New humanized anti-Fas antibody, useful for
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30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                         with abnormal Fas-Fas ligand systems
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98JP-0276882
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                                                 Human;
Tumour
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                                                                                      coding
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                                  antiarthritic; cardiant; monoclonal antibody; keloid; arthritis; Growth Factor-beta II receptor; TGF-beta II receptor; atopy; transduction inhibition; tissue fibrosis; atherosclerosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human monoclonal antibodies recognizing human TGF-beta II receptor useful for treating TGF-beta associated diseases such as tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 12; Page 103-104; 118pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 438 BP; 103 A; 123 C; 111 G; 101 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sakamoto S, Kamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NISB ) JAPAN TOBACCO INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibrosis
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                                                                                                                                                                                                                                                                     in
ggcggagggaccaaggtggagatcaaa
                                                                     CAGCCTGAAGATTTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCCTCGGACGTTC
                                                                                                                        CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                                                                             GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTAATTTAAATTGGTATCAGCAG
                                                                                                                                                                                                                                                                                                                                                       ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-343825/36
                            GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                                         ccatcaaggttcagcggcagtgcatctgggacagaattcactctcacaatcagcagcctg
                                                                                                                                                              aaaccagggaaagcccctaagcgcctgatctatgctgcatccagttttgcaaagtggggtc
                                                                                                                                                                            AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                  gtcaccatcacttgccgggcaagtcagggcattagaaatgatttaggctggtatcagcag
                                                                                                                                                                                                                                                                                                                            atggacatgagggtccccgctcagctcctggggctcctgctgctctggttcccaggtgcc
                                                     cagcctgaagattttgcaacttattactgtctacagcataatagtaacccgctcactttc
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the present invention.
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99JP-0328681
                                                                                                                                                                                                                                                                                                                                                                                             86.4%;
                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                           Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
  387
                                                                                                                                                                                                                                                                                                                                                                                         2 334.2; Db 22
No. 1.4e-92;
                                                                                                                                                                                                                                                                                                                                                                                 33;
                                                                                                                                                                                                                                                                                                                                                                                                        22;
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12-MAR-2002

(first

entry)

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immunomodulatory molecule (AILIM). (I) is useful for modulating signal currents duction into a cell mediated by AILIM, for modulating proliferation of AILIM-expressing cells, for modulating proliferation of AILIM-expressing cells, and for inducing antibody-dependent cytokine from AILIM-expressing cells. (I) is useful for treating, or apoptosis of AILIM-expressing cells. (I) is useful for treating or prophylaxis of delayed type allergy. (I) is useful for treating and preventing various diseases associated with AILIM-mediated costimulatory transduction, and for inhibiting the onset and/or advancement of the diseases. (I) is useful for suppression, prevention and/or treatment of rheumatoid arthritis, multiple colorosis, autoimmune thyroiditis, allergic contact-type dermatitis, chronic inflammation, graft versus host reaction, graft versus host consolidates, inflammation, graft versus host reaction, graft versus host casease, immune rejection, disorders caused by abnormal intestinal culture colitis, pneumonia, hepatitis, mephritis, vasculitis, and consolidate immunity, specifically inflammatory intestinal disorders such as
   Best Loc
Matches
                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiallergic; antiller; neuroprotective; antithyroid; vasotropic; immunosuppressive; dermatological; antiinflammatory; hepatotropic; activation inducible lymphocyte immunomodulatory molecule; AILIM; monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus; multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis; allergic contact-type dermatitis; chronic inflammatory dermatosis; systemic lupus erythematosus; autoimmune disorder; inflammation; ss; graft versus host reaction; immune rejection; intestinal immunity; ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.
                                                                                                                                                                                                                        pancreatitis. (I) induces no serious immunorejection due to antigenicity to human, i.e., human anti-mouse antigenicity (HAMA) in a host. AAS99444-AAS99477 represent anti-human AILIM monoclonal antibody coding sequences and PCR primers of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel human antibody (I), preferably a human monoclonal antibody which binds to an activation inducible lymphocyte immunomodulatory molecule (AILIM). (I) is useful for modulating signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 45; Page 267-270; 300pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human monoclonal antibody that binds to activation inducible lymphocyte immunomodulatory molecule, useful for treating rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAM:
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30-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2001;
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)B; AAU74297.
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Similarity 90.7
51; Conservative
                                                                                                                                                                  974
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                                                                                                                                                               BP;
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2001JP-0099508
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                          85.1%;
90.7%;
                                                                                                                                                               Α.
                                                                                                                                                               282
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   0,
Score 329.4; DB 24
Pred. No. 5.6e-91;
0; Mismatches 36;
                                                                                                                                                            232 G;
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                                                                                                                                                               0 other;
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ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC

The present sequence encodes a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigo (CTLA)-4. Antibodies of the invention are composed of a heavy chi

chain

Example 2; Fig 22r; 157pp; English.

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RESULT
AAA46899
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                                                        Novel antibodies capable of binding (CTLA)-4 containing specified heavy for treating, e.g. immune disorders
                                                                                                     WPI; 2000-442647/38
P-PSDB; AAY93735.
                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                 Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                          03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA46899
                                                                                                                                              Hanson
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(ABGE-)
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                                                                                                                                                                                                                                                                                                                                              proliferative
                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding
                                                                                                                                                                                                23-DEC-1998;
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                                                                                                                                             Ŋ,
                                                                                                                                                                  ABGENIX INC
                                                                                                                                                                             PFIZER INC
                                                                                                                                    JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                             disorder; autoimmune disease; diabetes; graft rejection; disorder; cancer; immunodeficient disorder; ss.
                                                                                                                                                                                                98US-0113647
                                                                                                                                                                                                                    99WO-US30895
                                                                                                                                                                                                                                                                                          Location/Qualifiers 67..714
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                                                                                                                                                                                                                                                                                                                                                                                    kappa chain
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                                                                     cytotoxic and light
                                                               and
                                                                                                                                             Hanke
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                                                                      T-lymphocyte antigen chain sequences, use
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                                                                      sequences, useful
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Best Local S
Matches 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.
                                                                                                                                                                                                               Complementarity Old World ape; (
 WPI; 2000-023265/02
                                                                                                                                   04-NOV-1999
                                                                                                                                                                                                                                                    Nucleotide sequence of chimpanzee Vkappa cDNA clone 46-14.
                                                                                                                                                                                                                                                                                                                                   AAZ39327 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 714 BP; 188 A; 199 C; 173 G; 154 T; 0 other;
                                                                               28-APR-1998;
                                                                                                         28-APR-1999;
                                                                                                                                                             WO9955369-A1
                                                                                                                                                                                    Pan troglodytes
                                                                                                                                                                                                                                                                                15-FEB-2000
                                                    (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                   361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGCCTGAAGATTTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCCAAGGGACCAAGGTGGAAATCAAA 387
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Matches 348
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                                                                                                Complementarity Old World ape;
                                                                                                                                        Nucleotide sequence of Cynomologous Vkappa cDNA clone 4-10.
                                                                                                                                                                                                                            AAZ39340 standard;
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                                                                     Macaca cynomolgus
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Old World monkey; an
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antigen-binding
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              Human
                                       03-DEC-1997
                                                                                           AAT73441 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antibodies containing donor non-human primate acceptor f humans -
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DB; AAY56672, AP
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           immunoglobulin light
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                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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transgenic; mouse; CD4; antibody; autoimmune; inflammatory;
transplant rejection; ss.
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                                                CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                               CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                               AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                            AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
                                 cagcctgaagattttgcaacttactattgtcaacaggctaatagtttcccgtacactttt
                                                                                                ccatcaaggttcagcggcagtggatctgggacagatttcactctcaccatcagcagcctg
                                                                                                                                                            aaaccagggaaagcccctaagctcctgatctatgctgcatccagtttgcaaagtggggtc
                                                                                                                                                                                                                              gtcaccatcacttgtcgggcgagtcaggatattagcagctggttagcctggtatcagcat
                                                                                                                                                                                                                                                            GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG
                                                                                                                                                                                                                                                                                           agatgcgacatccagatgacccagtctccatcttccgtgtctgcatctgtaggagacaga
                                                                                                                                                                                                                                                                                                                                                                                                                           344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95US-0544404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          82.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 C;
                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 318.2; DB 1
Pred. No. 1.1e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ი</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by transgenic etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                             43;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 388;
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RESULT 1
AAV39239
 producing a human heterologous antibodies of multiple isotypes by undergoing isotype switching. The transgenic animals have human heavy and light chain transgenes. The transgenes are capable of functionally rearranging a heterologous diversity (D) gene in a variable-diversity-junction (V-D-J) recombination. The transgenes include a heavy chain transgene comprising at least one V, D and J gene segment, and one constant region gene segment. The immunoglobulin (Ig) light chain transgene comprises at least one V and J gene segment and one constant region gene segment. The gene segment and one constant region gene segment. The gene segment are heterologous to the transgenic animal. The antibody can be used to prevent efflux of neutrophils from vasculature. It can also be used to treat reperfusion injury. CD4 binding antibodies are used to reduce undesirable autoimmune reactions, inflammatory responses and rejection of transplanted organs. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic animal; human heterologous antibody; transgene; isotype switching; neutrophil efflux; reperfusion injury; CD4 bindin autoimmune reaction; inflammatory response; transplant rejection; acid induced lung injury; acute adult respiratory distress syndrome; ARDS; vasculitis; septic shock; allergic reaction; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV39239 standard;
                                              anti-IL-8 antibodies can reduce tissue damage and prolong survival in animal models of acute adult respiratory distress syndrome (ARDS) and acid induced lung injury. The anti-IL-8 antibodies can also be used fit the treatment of vasculitis, septic shock, allergic reactions (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus
                                                                                                                                                                                                                                                                                                                                               transgenic mouse hybridoma cell lines. The specification describes transgenic non-human animals, especially a mouse, which are capable
                                                                                                                                                                                                                                                                                                                                                                                  AAV39232-41 represent functional transcripts of a human anti-CD4 antibody. The sequences are isolated from 5 dif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridoma producing antibody specific for interleukin-8 prevent efflux of neutrophils from vasculature, and trea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-DEC-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-1998
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repertusion injury
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENP-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENPHARM INT
 388
                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 304; 452pp; English.
                                cystic
 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0758417
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A; 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used
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Query Match Best Local Similarity

8 8 8 . 28;

Score Pred.

318.2; No. 1.

2; DB 19; 1.1e-87;

Length

388;

The specification describes transgenic animals that are capable of producing a heterologous antibody. The antibodies are isolated form hybridoma, comprising B cells, that is obtained from a transgenic mon having a genome comprising a human heavy chain transgene and a human

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                                                                                                                                                                                                                                                                                                                                           transgenic mouse; human heavy chain transgene; digoxin; PCR primer human light chain transgene; immortalized cell; immunoglobulin; Shinga-like toxin; autoimmune disease; cancer; infectious disease;
                                                                                 Novel transgenic antibodies
                                                                                                                                                                                                                                                                                                                                                                                Transgenic animal; heterologous antibody; hybridoma;
                                                                                                                                                                                                                                                                                                                                                                                                       Partial nucleotide sequence
                                                                                                                       WPI; 1999-551219/46
                                                                                                                                                                                              13-MAR-1998;
                                                                                                                                                                                                                      12-MAR-1999;
                                                                                                                                                                                                                                                                    W09945962-A1
                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                transplant rejection; blood disorder; coagulation disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                               24 - NOV - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ21993 standard;
                                                          Example 41; Page
                                                                                                                                           Lonberg N,
                                                                                                                                                                      (GENP-) GENPHARM INT
                                                                                                                                                                                                                                              16-SEP-1999.
                                                                                                                                                                                                                                                                                             Homo
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                                                                                                                                                                                                                                                                                             sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ccatcaaggttcagcggcagtggatctgggacagatttcactctcaccatcagcagcctg
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                                                                                                                                              Fishwild
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                                                                                                                                                                                                                     99WO-US05535
                                                                                                                                                                                              98US-0042353
                                                          305; 484pp; English.
                                                                                              non-human animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                       INC
                                                                                                                                              DM,
                                                                                                                                              Ball
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP
                                                                                                                                                                                                                                                                                                                                                                                                        for a functional transcript 10C5-kappa.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                387
                                                                                              used
                                                                                               6
                                                                                               produce heterologous
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                                                                                                                                                                                                                                                                                                                                                                               B cell;
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                                                                                                                                                                                                                                                                                                                                                                      primer;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       light chain transgene. The B cells are fused to immortalized cells suitable for generating a hybridoma, which produces a detectable amount of an immunoglobulin that specifically binds digoxin or Shinga-like toxin. B cells from transgenic animals can be used to generate hybridomas expressing monoclonal high affinity human sequence antibodies. Antibodies produced from the transgenic animals of the invention can be used to treat human diseases, e.g. autoimmune diseases, cancer, infectious disease, transplant rejection, blood disorders such as coagulation disorders and other diseases. The present sequence represents a partial nucleotide sequence for a functional transcript used in the course of the invention.
WO200029583-A2
                                                                                                                                                                                                                                                                                            AAA27390 standard;
                                   mat_peptide
                                                               sig_peptide
                                                                                                                                               Homo sapiens
                                                                                                                                                                                       Human;
                                                                                                                                                                                                                                         16-AUG-2000
                                                                                                                                                                                                                                                                   AAA27390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 388
                                                                                                                                                                         infection;
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Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                            CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
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                                                                                                                                                                                                                                                                                                                                                            ggccaggggaccaagctggagatcaaa
                                                                                                                                                                                                                                                                                                                                                                                                                cagcctgaagattttgcaacttactattgtcaacaggctaatagtttcccgtacactttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtcaccatcacttgtcgggcgagtcaggatattagcagctggttagcctggtatcagcat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344;
                                                                                                                                                                                                               IGFAM-10
                                                                                                                                                                                      immunoglobulin; IGFAM-10; IGFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                         inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                        (first entry)
                                                       /product=
19..84
                                                                                                                                                                                                               1mmunoglobulin
                       /*tag=
85..729
/*tag=
                                                                                                       Location/Qualifiers
19..732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                            CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; 107 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.2%;
                                                    ъ
                                                                                                                                                                                                                                                                                             936
                                                                                                                                                                        haematopoiesis;
                                                                              "IGFAM-10"
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Pred. No. 1.1e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                            coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                       387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 T; 0 other;
                                                                                                                                                                       immune disorder; cancer;
; AIDS; allergy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; DB 20;
1.1e-87;
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IGFAM-10 gene, which was isolated from a cDNA library of colon cc tissue. It is expressed in reproductive, gastrointestinal and cc cardiovascular tissue, where cancer and inflammation are common. The cc gene, protein, its antibodies, agonists and antagonists are suitable for cc diagnosing and treating many diseases, including cancer, immune system cc disorders (such as inflammation, AIDS, allergies, anaemia, crohn's cc arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's cc disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, cc multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, csystemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and chaematopoietic cancer (such as leukaemia) and infections caused by colored and constructions of sactoria, viruses, fungi or parasites.
                                                              Query Match
Best Local Sin
Matches 352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1998;
22-DEC-1998;
07-APR-1999;
                                                                                                                                                                                                                                                                                                                    Immunoglobulin superfamily proteins, i protein is useful for preventing and altered levels of the protein such as
                                                             Sequence
                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAY96298
                                                                                                                                                                                                                                                                                                                                                                                                                           Yue
                                                                                                                                                                                                                                                                                                                                                                                                               Lu DAM,
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             Similarity
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Lal
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                                                              936
 Conservative
                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                             P,
                                                                                                                                                                                                                                                                               99-100; 105pp;
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98US-0113635.
99US-0128194.
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Hillman
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            82.2%;
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Score 318; DB 21;
Pred. No. 1.7e-87;
0; Mismatches 35;
                                                                                                                                                                                                                                                                                 English.
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Yang J;
                                                              214 G;
                                                                                                                                                                                                                                                                                                                     the agonist and antagonist of the treating disorders associated wis cancer, immune system disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
                                                                                   CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGG---ACG
                                                                                                                                         AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGGTC
                                                                                                                                                                                                                                                                                                      GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTAATTTAAATTGGTATCAGCAG
                                                                                                                                                                                                                                                                                                                                                                           AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
                                 TTCGGCCAAGGGACCAAGGTGGAAATCAAA
                                                                                                                                                                              CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                                                                                                                                                    gtcaccatcacttgccgggcaagtcagagcattagcagctatttaaattggtatcagcag
                                                                                                                                                                                                                                                                                                                                                        agatgtgacatccagatgacccagtctccatcctccctgtctgcatctgtaggagacaga
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AAA27389
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Query Match
Best Local Similarity
Matches 343; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-1998;
22-DEC-1998;
07-APR-1999;
                                                                                   tissue. It is expressed in reproductive, gastrointestinal and immune and haematopoietic tissue, where cancer and inflammation are common. The gene, protein, its antibodies, agonists and antagonists are suitable for diagnosing and treating many diseases, including cancer, immune system disorders (such as inflammation, AIDS, allergies, aneemia, arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, systemic lupus erythematosus and ulcerative colitis), complications of cancer, haemodialysis and extracorporeal circulation, trauma and haematopoietic cancer (such as leukaemia) and infections caused by bacteria, viruses, fungi or parasites.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Yue
                                                                  Sequence 817
                                                                                                                                                                                                                                              The present sequence is the human immunoglobulin superfamily protein IGFAM-9 gene, which was isolated from a cDNA library of breast tumou
                                                                                                                                                                                                                                                                                     Claim 9;
                                                                                                                                                                                                                                                                                                                         Immunoglobulin superfamily proteins, the agonist and antagonist of the protein is useful for preventing and treating disorders associated with altered levels of the protein such as cancer, immune system disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immunoglobulin; IGFAM-9; IGFAM; immune disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IGFAM-9
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                                                                                                                                                                                                                                                                                                                                                                                                                     Lu DAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection; inflammation; haematopoiesis; AIDS; allergy; ss
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DB; AAY96297.
                                                                                                                                                                                                                                                                                                                                                                                                                     Tang
Lal
                                                                                                                                                                                                                                                                                      Page 99;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     P,
                                                               BP; 202 A; 237 C; 197 G; 181 T; 0 other;
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98US-0113635.
99US-0128194.
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Hillman
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11..76
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11..721
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            81.8%;
88.6%;
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0;
            Score 316.6; DB : Pred. No. 4.4e-87
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Yang J;
 Mismatches
                        DB 21;
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44;
                         Length
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Gaps
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Disclosure; Fig 4-5; 46pp; Japanese
                         Human anti-hepatitis B surface antigen antibody gene - can used to produce L and H chains of the antibody in large qua
                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                                                                                                                                               AAQ49943 standard; cDNA; 1066
                                                                WPI; 1993-336913/42.
                                                                                  Arima K,
                                                                                                                        30-MAR-1992;
                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                           Antibody; Al
HB; surface
                                                                                                                                                                                                                                                                                                                                      Human anti-HBs light chain.
                                                                                                                                                                                                                                                                                                                                                                             AAQ49943;
                                                       P-PSDB; AAR42065.
                                                                                                                                           30-MAR-1993;
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                                                                                  Kurihara T,
                                                                                                                                                                                                                                                                                                                     Ab;
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99..740
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33..98
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/note= "claim
                                                                                                                                                                                                                                                                                                           heavy;
                                                                                   Matsukura S,
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Best Local S
Matches 343
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                                                                                                                                                                                                                                                                                                                       Sequence 1066 BP; 338 A; 274 C; 240 G; 214 T; 0 other;
333
                                                                             273
                                                                                                 241
                                                                                                                    213
                                                                                                                            181 AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                           301
                                                                                                                                                                                           y Match 81.8%;
Local Similarity 88.6%;
hes 343; Conservative
                                                                           CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                  CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                       aaaccagggaaagtccctaagcgcctgatctatgctgcatccagtttgcaaagtggggtc
                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                        Score 316.6; DB 14; Length 1066; Pred. No. 4.9e-87; 0; Mismatches 44; Indels 0;
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Search completed: September 23, 2002, 17:58:50 Job time: 7014 sec

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 57, Appl Sequence 57, Appl	000	Sequence 31, Appl Sequence 31, Appl Sequence 22604, A		27, 27, 15,	62, 27, A	2087, 816, #	29, 192, 2087	Sequence 121, App Sequence 405, App Sequence 44, Appl Sequence 44, Appl	e 3, e 12; e 12;	Sequence 3, Appli Sequence 5, Appli	Description

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NAME/KEY: mat_peptide;
LOCATION: 67..387;
SEQUENCE DESCRIPTION: SEQ ID:
US-09-019-441-3
                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-198
CLASSIFICATION: CUnknown>
                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REGISTRATION NUMBER: 35,030
                                                                                          MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 012712-502
TELECOMMUNICATION INFORMATION:
TELEPHUNE: (703) 836-6620
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LOCATION:
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STATE: Virginia
COUNTRY: United States
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7 US-10-066-543-186
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7 US-09-844-684-13
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9 US-08-728-463-206
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Sequence 13, Appl
Sequence 22603, A
Sequence 22603, A
Sequence 22603, A
Sequence 206, App
Sequence 206, App
Sequence 206, App
Sequence 8123, Ap
Sequence 8123, Ap
Sequence 8123, Ap
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App
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Query Match

100.0%;

Score 387;

DB

14;

Length 387;

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LENGTH: 387

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (1)...(67)
NAME/KEY: matt_peptide
LOCATION: (67)...(387)
NAME/KEY: CDS
LOCATION: (1)...(387)
LOCATION: (1)...(387)
US-09-292-053-5
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SOFTWARE: Pate
SEQ ID NO 5
FRIGHTH: 387
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                                                                                                                                   Query Match 100.0%; Score 387; DB 16; Best Local Similarity 100.0%; Pred. No. 7.5e-109; Matches 387; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: REFF, MITCHELL E.
APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: NACAURA, TAKEHIKO
APPLICANT: NAKAWURA, TAKEHIKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND TITLE OF INVENTION: THEREOF AS THERAPEUTICS
FILE REFERENCE: 23522.0699
CURRENT APPLICATION NUMBER: US/09/292.053
CURRENT FILING DATE: 1999-04-14
PRIOR APPLICATION NUMBER: 08/803,085
PRIOR FILING DATE: 1997-02-20
NUMBER OF SED ID NOS: 39
COURMERS OF SED ID NOS: 39
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PRIOR APPLICATION NUMBER: 09/023,715
PRIOR FILING DATE: 1998-02-13
PRIOR PPLICATION NUMBER: 08/819,866
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEO ID NOS: 3
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 19040
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US-09-343-485A-3
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC TITLE OF INVENTION: MAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION A TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME FILE REFERENCE: 037003-0275807
CURRENT APPLICATION NUMBER: US/09/343,485A
CURRENT FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: REFF, MITCHELL R.
APPLICANT: BARNETT, RICHARD S.
APPLICANT: MCLACHLAN, KAREN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                              1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                     GGCCAAGGGACCAAGGTGGAAATCAAA 387
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                                                          AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
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                                           aaaccaggaaaagctcctaagctcctgatctatgttgcatccagtttgcaaagtggggtc
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RESULT 5 US-09-499-662-125

Sequence 125, Application US/09499662 GENERAL INFORMATION: APPLICANT: Serizawa, Nobufusa APPLICANT: Haruyama, Hideyuki

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; TYPE: DNA; ORGANISM: Homo sapiens US-09-408-646-125
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APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Tohru
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LENGTH: 729
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Anti-Fas Antibodies FILE REFERENCE: 990540/HG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 165
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             GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                          CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATTAGTACCCCTCGGACGTTC
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ggccaagggaccaaggtggaaatcaaa
                                                         caacctgaagattttgcaacttactactgtcaacagagttacagtacccctcgaacgttc
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Pred. No. 7.2
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APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Tamaki, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
CURRENT APPLICATION NUMBER: US/09/499,662
CURRENT FILING DATE: 2000-02-09
EARLIER APPLICATION NUMBER: US 09/053,583
EARLIER FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 125
LENGTH: 729
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PCT-US01-18569-121
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-499-662-125
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                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 121
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Best Local
                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US01/18569
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,467
PRIOR FILING DATE: 2000-06-07
                                                                                                                                                                                                                                                APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA133PCT
                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4360
                                                                                                         LENGTH: 11
TYPE: DNA
                                                                                      ORGANISM: Homo sapiens
                            OTHER INFORMATION: n
                                                                            FEATURE:
LOCATION: (424)
                 NAME/KEY:
                                            LOCATION:
                                                            NAME/KEY: SITE
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              SITE
                                            (302)
                                                                                                                                                                                                                                                                                                           Application PC/TUS0118569
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                           equals a,t,g,
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Pred. No. 7.2e-95;
0; Mismatches 28
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NAME/KEY: SITE
LOCATION: (201)
OTHER INFORMATION: n
NAME/KEY: SITE
LOCATION: (792)
OTHER INFORMATION: n
US-09-760-479-405
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; LOCATION: (1103)
; OTHER INFORMATION: n
PCT-US01-18569-121
                                                                                                                                                 Prior application data removed -
NUMBER OF SEQ ID NOS: 946
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 405
LENGTH: 812
                                                                                                                                                                                                                       Sequence 405, Application US/09760479
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ53
CURRENT APPLICATION NUMBER: US/09/760,479
CURRENT FILING DATE: 2001-01-16
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Best Local S
Matches 351
                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                         FEATURE:
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Pred. No. 8.2e-94;
7; Mismatches 29;
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Query Match

86

Score

335.2;

DВ

30;

Length 812

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RESULT 8
US-09-834-366-44
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                                                                                           Query Match
Best Local S
Matches 333
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PRIOR FILING DATE: 2000-04-18
NUMBER OF SEQ ID NOS: 52153
SOFTWARE: Patent.pm
SEQ ID NO 44
LENGTH: 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 44, Application US/09834366
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dumas Milne Edwa
                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 81.US2.REG
CURRENT APPLICATION NUMBER: US/09/834,366
CURRENT FILING DATE: 2001-04-13
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TITLE OF INVENTION: ESTS and Encoded Human
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                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 28.498
LOCATION: 28.93
COTHER INFORMATION: Score 13.600003811697
OTHER INFORMATION: see LGLLLLWIRGARC/DI
                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                     FEATURE:
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                                                                                               Conservative
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Pred. No. 1e-9
26; Mismatches
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ches 31;
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LOCATION: 28..498
NAME/KEY: Sig_peptide
LOCATION: 28..93
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 13.6000003814697
OTHER INFORMATION: seq LGLLLLWLRGARC/DI
US-60-197-873-44
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US-60-197-873-44
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APPLICANT: Tanaka, Hiroaki
APPLICANT: Dunas Milne Edwar:
APPLICANT: Jobert, Severin
APPLICANT: Giordano, Jean-Yv
TITLE OF INVENTION: ESTs and
FILE REFERENCE: 81 US1 PRO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 44
LENGTH: 500
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Best Local
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CURRENT FILING DATE: 2000-04-18
NUMBER OF SEO ID NOS: 52153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                            gtcaccatcacttgccgggcaagtcagrgcattakcrgctwtttaamttggtatcagcrs
                                                                                                                           agatgtgacatccagatgacccagtctccatcctccctgtctgyatctgtgggagacaga
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                                                                                                                                                                                                                                                                     Score 331.8; DB Pred. No. 1e-91;
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; LOCATION: (39)...(746); NAME/KEY: 3'UTR; LOCATION: (750)...(974); NAME/KEY: 51g_peptide; LOCATION: (39)...(104) US-09-859-053-29
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Best Local Similarity
Matches 351; Conserv
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TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM.
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-99508
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2000-05-18
NUMBER: OF SEQ. ID NOS: 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tsuji, Takashi
APPLICANT: Tezuka, Katsu
APPLICANT: Hori, Nobuaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)...(38)
NAME/KEY: CDS
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ccatcaaggttcagcggcagtggatctgggacagatttcactctcaccatcagcagcctg
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90.7%;
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Pred. No. 7.4e
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36;
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; Prior application data removed - re
; NUMBER OF SEQ ID NOS: 946
; SOETWARE: Patentin Ver. 2.0
; SEQ ID NO 192
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-760-479-192
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Sequence 192, Application US/09760479
SEQUENCE INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ53
CURRENT APPLICATION NUMBER: US/09/760,479
CURRENT FILING DATE: 2001-01-16
CURRENT FILING DATE: 2001-01-16
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Matches
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APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-765
CURRENT APPLICATION NUMBER: US/09/289,768
CURRENT FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 39996
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 2.
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PRIOR APPLICATION NUMBER: 09/289,768
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 39996
SOFTMARE: FastSEQ for Windows Version 3.
SEQ ID NO 2087
LENGTH: 391
TYPE: DNA
ORGANISM: Homo sapiens
US-09-939-397-2087
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Sequence 2087, Applia
GENERAL INFORMATION:
APPLICANT: Hyseq, I
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LENGTH: 391
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                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/939,397 CURRENT FILING DATE: 2001-08-24
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agatgtgacatccagatgacccagtctccatcctccctgtctgcatctgtaggagacaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                               AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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Pred. No. 2.9e-90;
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Pred. No. 2.9e-90;
0; Mismatches 35;
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                                                                                                                                                                                                                                                                                               3.0
                                                                                                                                 35;
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PRIOR EILING DATE: 1999-09
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-09
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE: 1999-09
NUMBER OF SEQ ID NOS:
SOFTWARE: PERL Progra
SEQ ID NO 816
LENGTH: 549
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GENERAL INFORMATION
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                                                           PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: 60/168,614
PRIOR EILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/168,611
PRIOR TILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/168,613
PRIOR APPLICATION NUMBER: 60/168,613
PRIOR FILING DATE: 1999-12-02
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APPLICANT:
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                                                                                                                                                                           PRIOR APPLICATION NUMBER: 60/168,599
PRIOR FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: 60/168,197
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/665,486
CURRENT FILING DATE: 2000-09-20
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: ANTIGEN RECOGNITION MOLECULES FILE REFERENCE: PT-0076 US
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                                PERL Program
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Yu, Jimmy Y.
Greenawalt, Lila B.
Panzer, Scott R.
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Spiro, Peter A.
Banville, Steve C.
Bratcher, Shawn R.
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Wright, Rachel J.
Chen, Wensheng
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Fong, Willy T.
                                                                                                                                                                                                                                                                                                                                                                                                                          Yap, Pierre E.
Stockdreher, Theresa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jennifer L
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APPLICANT: Lincoln, Stephen E.
APPLICANT: Russo, Frank D.
APPLICANT: Spiro, Peter A.
APPLICANT: Spiro, Peter A.
APPLICANT: Spiro, Peter A.
APPLICANT: Banville, Steve C.
APPLICANT: Bratcher, Shawn R.
APPLICANT: Dufour, Gerard E.
APPLICANT: Cohen, Howard J.
APPLICANT: Cohen, Howard J.
APPLICANT: Rosen, Bruce
APPLICANT: Chen, Waright, Rachel J.
Chen, Wensheng
Lilu, Tommy
APPLICANT: Rosen, Bruce
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Shah, Purvi
APPLICANT: Hilman, Jennifer L.
TITLE OF INVENTION: ANTIGEN RECOGNITION MOLECULES
FILE REFERENCE: PT-0099 P
CURRENT APPLICATION NUMBER: US/60/168,599
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 737
SOFTWARE: PERL Program
LENGTH: 549
TYDE: NNA
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ORGANISM: Homo saple...
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte If
NAME/KEY: unsure
LOCATION: 488
OTHER INFORMATION: a, t, c
US-09-665-486-816
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Best Local S
Matches 349
TYPE: DNA
ORGANISM: Homo sapiens
FENTURE:
NAME/KEY: misc_feature
OfHER INFORMATION: Incyte I
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                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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Pred. No. 5.9e-90;
0; Mismatches 38
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Best Local Similarity
Matches 349; Conserv
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  380
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                                                           CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                           CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                                                                                                                                          AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                            GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTAATTTAAATTGGTATCAGCAG
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ggccaagggaccaaggtggagatcaaa
                       GGCCAAGGGACCAAGGTGGAAATCAAA 387
                                                                                             ccatcaaggttcagcggcagtggatctggcacagattacactctcaccatcagcagcctg
                                                                                                                                             aaaccagggaaagcccctaagctcctgatctatgctgcatccaagttacacaccggggtc
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                                             cagcctgaagactttgcaacttattactgtctgcaagattacagttaccctcggacgttc
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Pred. No. 5.9e-90;
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Search completed: September 23, 2002, 19:47:27 Job time: 7022 sec

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Result
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Listing first 45 summaries
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/cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq:*
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            DB
6 US-10-216-484-125
6 US-10-206-008-405
6 US-10-206-008-405
6 US-10-206-008-192
7 US-10-153-382-18
7 US-10-214-403-186
7 US-10-214-403-186
7 US-10-214-403-186
7 US-09-831-805A-29
5 US-09-831-805A-29
5 US-09-831-805A-20
7 US-10-158-646-55
7 US-10-158-646-55
7 US-10-158-646-55
7 US-10-158-646-56
7 US-10-158-646-56
7 US-10-158-646-56
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7 US-10-146-502-181
7 US-09-335-6978-116
7 US-09-335-697
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                              Sequence 3, Appli
Sequence 125, App
Sequence 192, App
Sequence 115, Appl
Sequence 116, Appl
Sequence 116, Appl
Sequence 2025, Appl
Sequence 29, Appl
Sequence 29, Appl
Sequence 21, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 55, Appl
Sequence 55, Appl
Sequence 56, Appl
Sequence 110, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 11, Appl
Sequence 111, Appl
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278.6	278.8	279	279.2	279.4	279.4	280.4	281.8	281.8	281.8	283.4	284.8	284.8	285	286.2	287.4	287.8	289.2	295	295
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Sequence 36, Appl	Sequence 12346, A	Sequence 5398, Ap	Sequence 7569, Ap	Sequence 1, Appli	Sequence 1, Appli	Sequence 68, Appl	Sequence 42, Appl	Sequence 33; Appl	Sequence 27, Appl	Sequence 39, Appl	Sequence 1918, Ap	Sequence 1918, Ap	Sequence 30, Appl	Sequence 31, Appl	Sequence 2039, Ap	Sequence 24, Appl	Sequence 78, Appl	Sequence 101, App	Sequence 65, Appl

ALIGNMENTS

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RESULT 1
US-10-103-686-3
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GENERAL INFORMATION:
APPLICANT REFF, Mitchell E.
KLOETZER, William S.
NAKAMURA, Takehiko
TITLE OF INVENTION: GAMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                               TELEFAX: (703) 83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/103,686
ETILING DATE: 25-Mar-2002
CLASS_ETICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,03
REFERENCE/DOCKET NUMBER: CTELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/803,085 FILING DATE: 20-FEB-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
                   FEATURE:
                                                                                 FEATURE:
                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                    MOLECULE TYPE:
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STATE: Virginia
COUNTRY: United States
                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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NAME/KEY:
                                       LOCATION:
                                                               NAME/KEY:
                                                                                                                          TOPOLOGY:
                                                                                                                                                                                      LENGTH: 387 base pairs
                                                                                                    DNA (genomic)
                                                                                                                        linear
mat_peptide
                                                               CDS
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                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-216-484-125
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US-10-216-484-125
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                                                                                     Query Match
Best Local S
Matches 359
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 125, Application US/10216484 GENERAL INFORMATION:
                                                                                                                                                                                       SEQ ID NO 125
LENGTH: 729
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Best Local :
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/216,46 CURRENT FILING DATE: 2002-08-09 PRIOR APPLICATION NUMBER: US/09/499,662 PRIOR FILING DATE: 2000-02-09 PRIOR APPLICATION NUMBER: US 09/053,583 PRIOR FILING DATE: 1998-04-01
                                                                                                                                                                                                                                                                                                                         APPLICANT: Serizawa, Nobufusa
APPLICANT: Haruyama, Hideyuk
APPLICANT: Nakahara, Kaori
APPLICANT: Tamaki, Ikuko
APPLICANT: Takahashi, Tohru
                                                                                                                                                                                                                                                                                               APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 980126CIP/HG
                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
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                                  GGCCAAGGGACCAAGGTGGAAATCAAA 387
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             AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA
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387;
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                                                                                                                                                                                                                                                                                                                                   Haruyama, Hideyuki
Nakahara, Kaori
Tamaki, Ikuko
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Pred. No. 1.6e-93;
0; Mismatches 28;
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Pred. No. 3.6e-107;
Mismatches 0;
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US-10-206-008-405; Sequence 405; Applica GENERAL INFORMATION: APPLICANT: Rosen et PRIOR APPLICATION NUMBER: 09/760,479
PRIOR APPLICATION NUMBER: 09/7760,479
PRIOR APPLICATION NUMBER: 60/7179,065
PRIOR PILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/780,628
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: 60/214,886
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/217,487
PRIOR APPLICATION NUMBER: 60/227,787
PRIOR APPLICATION NUMBER: 60/227,788
PRIOR APPLICATION NUMBER: 60/225,758 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR CURRENT APPLICATION NUMBER: US/10/206,008 CURRENT FILING DATE: 2002-07-29 PRIOR PRIOR PRIOR FILE REFERENCE: PTZ53ClN TITLE OF INVENTION: Nucleic Acids, Proteins, OR PELICATION NUMBER: 60/225,757
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/226,868
OR FILING DATE: 2000-08-22
OR APPLICATION NUMBER: 60/216,647
OR FILING DATE: 2000-07-07
OR FILING DATE: 2000-07-07
OR APPLICATION NUMBER: 60/215,267
OR APPLICATION NUMBER: 60/216,880
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/216,880 OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/220,963
OR FILING DATE: 2000-07-26
OR APPLICATION NUMBER: 60/217,496
OR FILING DATE: 2000-07-11
OR APPLICATION NUMBER: 60/225,447
OR APPLICATION NUMBER: 60/218,290
OR APPLICATION NUMBER: 60/218,290
OR APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-12-08
APPLICATION NUMBER: 60/235,
FILING DATE: 2000-09-27
APPLICATION NUMBER: 60/234,
FILING DATE: 2000-09-21 FILING APPLICATION FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/251,869 FILING DATE: 2000-07-07 APPLICATION NUMBER: 60/225, FILING DATE: Rosen et al DATE: Application NUMBER: 2000-07-14 2000-09-2002-07 US/10206008 60/234,223 60/235,834 and Antibodies

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                                  OR APPLICATION NUMBER: 09/760,479
OR FILING DATE: 2001-01-16
OR APPLICATION NUMBER: 60/17,065
OR FILING DATE: 2000-01-31
OR APPLICATION NUMBER: 60/210,628
OR APPLICATION NUMBER: 60/214,886
OR FILING DATE: 2000-02-04
OR APPLICATION NUMBER: 60/217,487
OR APPLICATION NUMBER: 60/217,487
OR APPLICATION NUMBER: 60/225,758
OR APPLICATION NUMBER: 60/220,963
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/217,496
OR FILING DATE: 2000-07-12
OR APPLICATION NUMBER: 60/217,496
OR APPLICATION NUMBER: 60/217,496
OR APPLICATION NUMBER: 60/225,447
OR APPLICATION NUMBER: 60/218,290
OR FILING DATE: 2000-08-14
OR APPLICATION NUMBER: 60/218,290
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IN APPLICATION NUMBER: 60/246,475
OR FILING DATE: 2000-11-08
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OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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nilarity 90.2%;
Conservative
                        NUMBER: 60/225,757
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Pred. No. 2.2e-91;
7; Mismatches 31;
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APPLICATION NUMBER: 60/215,135
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APPLICATION NUMBER: 60/225,266
FILING DATE: 2000-08-14
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FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/225,759
FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/225,213
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APPLICATION NUMBER: 60/249,245
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APPLICATION NUMBER: 60/249,212
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APPLICATION NUMBER: 60/246,474
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APPLICATION NUMBER: 60/241,787
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DR APPLICATION NUMBER: 60/241,826
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DR APPLICATION NUMBER: 60/241,786
DR FILLING DATE: 2000-10-20
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FILING DATE: 2000-09-14
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APPLICATION NUMBER: 60/232,397
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APPLICATION NUMBER:
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RESULT 5
US-10-153-382-18
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GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 714
                                                                                                                   PRIOR APPLICATION NUMBER: 60/293042 PRIOR FILING DATE: 2001-05-23
                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
                                                                                               NUMBER OF SEQ ID NOS: 39
TYPE: DNA
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360 315 300 240 195 180

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; SEQ ID NO 15; LENGTH: 728; TYPE: DNA; ORGANISM: Homo s
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US-10-040-244-15
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Best Local
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                                                                                                                                                                                                                                 TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD FILE REFERENCE: 021286/0272501

CURRENT APPLICATION NUMBER: US/10/040,244

CURRENT FILING DATE: 2002-06-17

PRIOR APPLICATION NUMBER: 60/200,601

PRIOR FILING DATE: 2000-4-28

PRIOR APPLICATION NUMBER: PCT/US01/13672

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: 09/844,684

PRIOR FILING DATE: 2001-04-27

PRIOR APPLICATION NUMBER: 09/844,684

PRIOR FILING DATE: 2001-04-27

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KIRIN BEER KABUSHIKI KAISHA
APPLICANT: FORCE, WALKER F.
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI
61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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                                                                                         Conservative
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                                                                                      Score 323; DB 7;
Pred. No. 1.1e-87;
0; Mismatches 40
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Pred. No. 1.2e-88;
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                                                                                                                 Length 728;
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LENGTH: 514
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Best Local
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APPLICANT:
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; TYPE: DNA; Homo sapiens; ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCE FILE REFERENCE: 210121.563C1
CURRENT APPLICATION NUMBER: US/10/214,403
CURRENT FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 3420
SOFTWARE: FastSEQ for Windows Version 4.0
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                     181 AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                               121 GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTAATTTAAATTGGTATCAGCAG
                                                                                                                                                                                                    61 AGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGA 120
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nes 346; Conserv
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aaaccaggaaaagttcctaagctcctgatctatgctgcatccactttgcaatctggggtc
                                                                                     gtcaccatcacttgccgggcgagtcagggcattagcaattatttagcctggtatcagcag
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Durham, Margarita
Stolk, John A.
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Carter, Darrick
Fanger, Gary R.
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APPLICANT: Lodes, Michael J.

APPLICANT: Secrist, Heather
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.

APPLICANT: Smith, Carole L.
APPLICANT: Durham, Margarita
APPLICANT: Stolk, John A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 21012.563C1
CURRENT APPLICATION NUMBER: US/10/214,403
CURRENT FILING DATE: 2002-08-06
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GENERAL INFORMATION:
APPLICANT Jiang, Yu
APPLICANT Chenault
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APPLICANT IN Jian
APPLICANT Forestst,
APPLICANT Secrist,
APPLICANT Carter,
APPLICANT Franger,
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US-10-214-403-186/c
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 186
LENGTH: 537
TYPE: DNA
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Best Local :
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                                                         CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
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CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCCTCGGACGTTC
                                                                                                                                      AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                                                                                                      GTCACCATCACTTGCCGGGCGAGTCAGGGCATTAGCCAATTATTTAGCCTGGTATCAGCAG
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Chenault, R
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RESULT 10
US-09-831-805A-29
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; ORGANISM: Homo sapiens
US-10-040-244-13
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US-10-040-244-13
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SEQ ID NO 13
LENGTH: 716
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KIRIN BEER KABUSHIKI KAISHA
APPLICANT: FORCE, WALKER F.
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI
ITILE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40.
FILE REFERENCE: 021286/0272501
CURRENT APPLICATION NUMBER: US/10/040,244
CURRENT FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 60/200,601
PRIOR FILING DATE: 2001-04-28
PRIOR APPLICATION NUMBER: PCT/US01/13672
PRIOR APPLICATION NUMBER: 09/844,684
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
RUMBER OF SEQ ID NOS: 17
RUMBER OF SEQ ID NOS: 17
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                                                                                 GGCCAAGGGACCAAGGTGGAAATCAAA 387
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                                                                   ggccaagggaccaaggtggagatcaaa
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Sequence 29, Application US/09831805A GENERAL INFORMATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC. APPLICANT: YUE, Henry APPLICANT: TANG, Y. Tom

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GENERAL INFORMÁTION:
APPLICANT: INCYTE PHARMACEUTICALS, IN
APPLICANT: YUE, Henry
APPLICANT: TANG, Y. Tom
APPLICANT: CORLEY, Neil C.
APPLICANT: GUEGLER, Karl J.
APPLICANT: GUEGLER, Gina A.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: LAL, Dyung Aina M.
APPLICANT: LAL, Preeti
APPLICANT: LAL, Preeti
APPLICANT: HILLMAN, Jennifer L.
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; OTHER INFORMATION: Incyte
US-09-831-805A-29
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CURRENT FILING DATE: 2002-08-26

PRIOR APPLICATION NUMBER: 09/195,853; unassigned; 60/113,635; 60/128,194

PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22; 1999-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: YANG, Junming TITLE OF INVENTION: IMMUNOGLOBULIN FILE REFERENCE: PF-0643 PCT
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ORGANISM: Homo sapiens
FEATURE:
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52; Conservative
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; OTHER INFORMATION: Incyte
US-09-831-805A-28
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APPLICANT: YUE, Henry
APPLICANT: TANG, Y. TOm
APPLICANT: CORLEY, Neil C.
APPLICANT: GUECLER, Karl J.
APPLICANT: GUECLER, Karl A.
APPLICANT: BAUGHN, Mariah R.
                                                                                                                                                                                                                                                                                        Sequence 20, Application US/09831805A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: P.
SEQ ID NO 28
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: YANG, Junming
TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-0643 PCT
CURRENT APPLICATION NUMBER: US/09/831,805A
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 09/195,853; unassigned; 60/11
PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22;
                                                                                                                                    APPLICANT:
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Best Local Similarity
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TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
FILE REFERENCE: PF-0643 PCT
CURRENT APPLICATION NUMBER: US/09/831,805A
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 09/195,853; unassigned; 60/113,635; 60/128,194
PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22; 1999-04-07
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              311
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GORGONE, Gina A.
BAUGHN, Mariah R.
LU, Dyung Aina M.
LAL, Preeti
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88.6%;
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Pred. No. 9.7e-86
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                   60/113,635;
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     1999-04-07
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                   60/128,194
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; OTHER INFORMATION: Incyte ID NO: 079785CB1
US-09-831-805A-20
                                       ; TYPE: DNA
; ORGANISM: Homo
US-10-040-244-11
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US-10-040-244-11
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SOFTWARE: PERL I
SEQ ID NO 20
LENGTH: 917
                                                                             NUMBER OF SEQ ID NOS: 1:
SOFTWARE: PatentIn Ver.
SEQ ID NO 11
LENGTH: 698
                                                                                                                                                                                                                                                                                                                            Sequence 11, Application US/10040244 GENERAL INFORMATION:
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Best Local
Query Match
                                                                                                                               PRIOR APPLICATION NUMBER: 60/200,601
PRIOR FILING DATE: 2000-4-28
PRIOR APPLICATION NUMBER: PCT/US01/13672
PRIOR FILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 09/844,684
PRIOR FILING DATE: 2001-04-27
NUMBER: 09/844,684
                                                                                                                                                                                                                                                                     APPLICANT: KIRIN BEER KABUSHIKI KAISHA
APPLICANT: FORCE, WALKER F.
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI
                                                                                                                                                                                                                                             TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOUTILE REFERENCE: 021286/0272501
                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/040,244
CURRENT FILING DATE: 2002-06-17
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ORGANISM: Homo sapiens
FEATURE:
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Pred. No. 1.2e-85;
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Sequence 48, Application US/09602148A
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Jiang, Yuqiu
ITITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.482
CURRENT APPLICATION NUMBER: US/09/602,148A
CURRENT FILING DATE: 2002-04-09
NUMBER OF SEQ ID NOS: 126
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 48
LENGTH: 944
TYPE: DNA
CREAKING ASSETS OF SERVICES AND ASSETS OF SERVICE
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US-09-602-148A-48
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Best Local Similarity 87.9%;
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Pred. No. 2.9e-84;
0; Mismatches 47;
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ches 47;
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Sequence 55, Application US/10158646

GENERAL INFORMATION:
APPLICANT: Lasek, Amy K.W.
APPLICANT: Sornasse, Thierry
TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
FILE REFERENCE: PA-0030-1 US
CURRENT APPLICATION NUMBER: US/10/158,646
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: 60/295,239
PRIOR APPLICATION NUMBER: 60/295,239
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEO ID NOS: 78
SOFTWARE: PERL Program
SEQ ID NO 55
LENGTH: 634
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 1039732.6
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Best Local Similarity 90.5
Matches 342; Conservative
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                                                                AGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAAGG
                                                                                                                  GTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCTGA 308
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90.5%;
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Search completed: September 23, 2002, 19:58:52 Job time: 7182 sec

time:

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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387
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    Issued_Patents_NA:*
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Copyright (c) 1993 - 2000
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-042-353-360
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US-08-634-223-16
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US-08-634-240-16
US-08-635-878-16
US-08-635-878-16
US-08-758-4178-220
US-09-042-353-93
US-08-758-4178-243
US-08-758-4178-243
US-08-646-367-2
US-08-646-367-13
US-08-646-367-13
US-08-646-367-13
US-08-648-376-18
US-08-634-223-18
US-08-634-223-18
US-08-634-223-18
US-08-634-400-18
US-08-634-400-18
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US-09-042-353-358

US-08-758-417A-206

US-08-157-101A-4
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Compugen Ltd
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308, App
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16, App1
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18, App1
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45	44	43	42	41	40	39	38	37	36	35	34	33	3 <b>2</b>	31	30	29	28
264.8	264.8	265	266.4	266.4	268	268.6	268.6	268.6	268.6	269	269.6	269.6	269.6	269.6	273.8	278.2	278.2
68.4	68.4	68.5	68.8	68.8	69.3	69.4	69.4	69.4	69.4	69.5	69.7	69.7	69.7	69.7	70.7	71.9	71.9
321	321	324	321	321	321	401	401	401	401	382	321	321	321	321	381	708	708
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US-09-240-274-104	US-09-240-274-98	US-08-378-939-17 .	US-09-240-274-216	US-09-240-274-107	US-09-240-274-105	US-08-082-842A-47	US-08-477-531B-47	US-08-472-788A-47	US-08-107-669D-47	US-08-836-561-70	US-09-240-274-222	US-09-240-274-221	US-09-240-274-218	US-09-240-274-102	US-08-621-751A-5	US-09-335-697B-18	US-08-770-057-18
Sequence 104, App	Sequence 98, Appl		Sequence 216, App	•	Sequence 105, App	Sequence 47, Appl	Sequence 47, Appl	47,	47,	Sequence 70, Appl	•	•	Sequence 218, App	Sequence 102, App	Sequence 5, Appli	Sequence 18, Appl	Sequence 18, Appl

## ALIGNMENTS

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; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-803-085-3
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US-08-803-085-3
                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 0127
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08803085
Patent No. 6011138
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
APPLICANT: KLOETZER, William S.
APPLICANT: NAKAMURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                     FEATURE:
                                                                                                                                     TOPOLOGY: 11
MOLECULE TYPE:
                                                                            NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 20-FEE CLASSIFICATION: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: United States ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                       NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: BURNS, DOANE, SWECKER & MATHIS P.O. Box 1404
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                                                                              CDS
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RESULT 2
US-09-042-353-358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Lonber
APPLICANT: Kay, R
                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
              FILING DATE: 16-DEC-
PRIOR APPLICATION DATA:
                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animo
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
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                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 13-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                               STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCCTGAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                   94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                 San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                           E: Townsend and Townsend and Crew LLP
Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lonberg, Nils
                               16-DEC-1992
                                                                                                                                                                                                                                                                                                     PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transgenic No. 6255458-Human Animals for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 387; DB 3; 100.0%; Pred. No. 8.4e-113;
                                               us 07/990,860
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us 08/053,131
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Best Local
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
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APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
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APPLICATION NUMBER:
FILING DATE: 02-DEC-
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 07-DE
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           CCATCAAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG
                                            AAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTC
                                                                         AAACCAGGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTC
                                                                                                        GTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTGGTATCAGCAG
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03-DEC-1993
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10-DEC-1993
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ER: 014643-009040US
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RESULT 3
US-08-758-417A-206
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GENERAL INFORMATION:
                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 206:
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 MOLECULE
SEQUENCE
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and
STREET: Two Embarcadero
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                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
TOPOLOGY: linear DULE TYPE: DNA DISCRIPTION:
                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                            NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
                                                                                                                                                                                                                                                                                      FILING DATE: 22-JUL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
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FILING DATE: 10-CCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-CCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/165,699 FILING DATE: 10-DEC-1993
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                                                                                             LENGTH: 388 base pairs
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Patent No. 580803
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Best Local :
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                                                                                         APPLICATION NUMBER: US/08/
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                   TELEPHONE:
                                                                           REFERENCE/DOCKET NUMBER:
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                   TELEFAX:
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                 202-822-0944
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TSURUOKA, NOBUO
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GENES

AND

EXPRESSION

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RESULT 5
US-08-217-918-1
; Sequence 1, Applica
; Patent No. 5506132
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (ger
US-08-157-101A-4
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Best Local
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                                                                                                                                                                                                                                                                         APPLICANT: LAKE, PHILIP
APPLICANT: OSTBERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
            ATTORNEY/AGENT INFORMATION:
NAME: Smith, Willaim M
REGISTRATION NUMBER: 30,223
                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
TELECOMMUNICAȚION INFORMATION:
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                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                               STREET: 379 Lytton Avenue CITY: Palo Alto STATE: California
                                                                                                                        SOFTWARE:
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                                                                                                                       PatentIn Release #1.0, Version #1.25
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88.6%;
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Pred. No. 1.9e-90;
0; Mismatches 44
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GENERAL A...

APPLICANT: Kay, Robert M.

APPLICANT: Kay, Robert M.

TITLE OF INVENTION: Transgenic No. 6255458-Huma...

TITLE OF INVENTION: Producing Heterologous Antibodic NUMBER OF SEQUENCES: 421

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

ADDRESSEE: Townsend and Center, Eighth Floor
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US-09-042-353-360
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US-08-217-918-1
                                                                                                                                                                                                                                                                  Patent No. 6255458
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                Sequence 360,
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Best Local Similarity
Matches 338; Conserv
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    STREET: TWO CITY: San Francisco
STATE: California
 CURRENT
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             SOFTWARE:
                                                                                                  COUNTRY:
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APPLICATION
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             Patentin Release #1.0,
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87.38;
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Pred. No. 4.2e-88;
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             Version #1.30
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Antibodies
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APPLICATION NUMBER:

US/09/042,353

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                                 Matches
                                             Query Match
Best Local (
                                                                                                                                                                                                                       TELEFAX: (415) 576-03
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PI
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 10-DEC-
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                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-OCT-PRIOR APPLICATION DATA:
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                              Local Similarity hes 337; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 09-MAI
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                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                         NAME: Apple, Randolph REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/161,739 FILING DATE: 03-DEC-1993
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1 ATGGACATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCCAGGTGCC 60
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                                                                                                                                                                           nucleic acid
                                                                                                                                                                                        439 base pairs
                                 Conservative
                                                                                                                                              linear
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02-DEC-1996
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10-OCT-1995
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18-MAR-1992
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23-JUN-1992
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87.1%;
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                              0;
                              Score 307; DB 4;
Pred. No. 1.4e-87;
0; Mismatches 50
                              50;
                                                            Length 439
                              Indels
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US-08-758-417A-208
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                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kay, Robe TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lonberg, Nils
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGCCTGAAGATTTTTGCGACTTATTACTGTCTACAGGTTTATTAGTACCCCTCGGACGTTC
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APPLICATION NUMBER: US 08/096,762 FILING DATE: 22-JUL-1993 APPLICATION NUMBER: US 08/053,131 FILING DATE: 26-APR-1993
                                                                                                                                                                                               APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/758,417A FILING DATE: 02-Dec-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
STATE: California
                                                                  APPLICATION NUMBER: US
FILING DATE: 18-NOV-199
                                                                                                                                APPLICATION NUMBER: US 08/165,699 FILING DATE: 10-DEC-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                 FILING DATE: 03-DEC-1
                                                                                                                                                                 FILING DATE: 09-MAR-1994
                                                                                                                                                                                 APPLICATION NUMBER: US 08/209,741
                                                                                                                 APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert M.
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1993
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LENGTH: 439 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID
US-08-758-417A-208
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FILING DATE: 16-DEC-1992
ATTORNEY_AGENT INFORMATION:
NAME: Serafin1, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE_POCKET NUMBER: 014643-009030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Best Local S
Matches 337
                                                                                                                                                                                                                  Sequence 16, Application US/08488376 Patent No. 5811524 GENERAL INFORMATION:
                                                                                  APPLICANT: BRAMS, PE
APPLICANT: CHAMAT, S
APPLICANT: PAN, L1-Z
APPLICANT: WALSH, Ed
APPLICANT: HEARD, Ch
APPLICANT: NEWMAN, R
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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nes 337; Conserv
                                         ADDRESSEE: Burns,
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Alexandria
Virginia
                             P.O. Box 1404
                                                                                   NEWMAN, ROLAND ANTHONY
AVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
AVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO
AVENTION: METHODS FOR THEIR MANUFACTURE AND
                                                                                                                                         WALSH, Edward E.
HEARD, Cheryl Janne
                                                                                                                                                                        BRAMS, Peter
CHAMAT, Soulaima Salim
PAN, L1-2hen
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                                         Doane,
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Pred. No. 1.4e-87;
0; Mismatches 50
                                           Swecker
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                                                                                     THERAPEUTIC USE THEREOF
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RESULT 9 US-08-634-223-16

Sequence 16, Application US/08634223 Patent No. 5840298

GENERAL INFORMATION: APPLICANT: BRAMS,

BRAMS, Peter

APPLICANT:

CHAMAT, Soulaima Salim PAN, Li-Zhen

WALSH,

Edward

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; LOCATION:
US-08-488-376-16
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/00 FILING DATE: 07-JUN-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Teskin, Robin L. REGISTRATION NUMBER: 35,030
                                                                                                                                                                                                                                                                                                                                                 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 126
                                                                                                                                                                                      GGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
                                                                                                                                                                                                                                                  ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCA 186
GGGACCAAGGTGGAAATCAAA
                           GGGACCAAGGTGGAAATCAAA 387
                                                      GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA
                                                                                                                              AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
                                                                                                                                                                          GGGAAAGCCCCTAAGCTCCTGATATATGCTGGATCCAATTTGCACCGTGGGGTCCCGTCA
                                                                                                                 AGGTTCAGTGGCGGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                         tch 78.6%; al Similarity 87.4%; 333; Conservative
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Pred. No. 1.3e-86;
0; Mismatches 48
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,223
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CITY: Alexandria
STATE: Virginia
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nes 333; Conserv
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STRANDEDNESS: sing
TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22313-1404
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              GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
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                                                                                                   AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT 306
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GAAGATTTTGCAACTTACTATTGTCAACAGGCTTACAGTACCCCCTGGACTTTCGGCCCA
                                                                                                                                     GGGAAAGCCCCTAAGCTCCTGATATATGCTGGATCCAATTTGCACCGTGGGGTCCCGTCA
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                                                                AGGTTCAGTGGCGGTGGATCTGGGACAGATTTCACTCTCACCATCAACAGTCTGCAACCT
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P.O. Box 1404
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VERVION: NEUTRALIZING HIGH AFFINITY HUMAN
VERVION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
VERVION: MCTHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
EQUENCES: 19
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87.4%;
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Pred. No. 1.3e-86;
0; Mismatches 48
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Best Local Similarity
Matches 333; Conserv
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Patent No. 5866125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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ATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATATTTAAATTGGTATCAGCAGAAACCA
                                            GACATCCAGATGACCCAGTCTCCCATCTTCCCTGTCTGCATCTGTAGGGGACAGAGTCACC 126
                                                                                                    ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCCAGATGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
                                                                                                                                                                                                                                                                                                                                      1: 705 base pairs nucleic acid
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P.O. Box 1404
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                                                                                                                                                                                                                                                                                                                                                                                                 (703) 836-2021
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PAN, Li-Zhen
                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                              linear
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87.4%;
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MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE TH
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                                                                                                                                                               Mismatches
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US-08-634-400-16
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STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/634,400
FILING DATE: O7-UN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
BEGITERSTION TUNNERSE 32.00
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Patent No. 5939068
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INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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APPLICANT: WALSH, Edward E.
APPLICANT: WALSH, Edward E.
APPLICANT: HEARD, Cheryl Janne
APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: MEDUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                   MOLECULE TYPE:
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                                                                                  STRANDEDNESS:
TOPOLOGY: lir
                                NAME/KEY:
                LOCATION:
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                                                                 DNA (genomic)
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US-08-635-878-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NEWMAN, Roland Anthony
TITLE OF INVENTION: MEUTRALIZING HIGH AFFINITY HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN
TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC US
NUMBER OF SEQUENCES: 19
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 07-JUN-1995
                                                                      FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                              STREET: P.O. Box
CITY: Alexandria
STATE: Virginia
                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                             COUNTRY: United States ZIP: 22313-1404
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                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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P.O. Box 1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WALSH, Edward E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAMAT, Soulaima Salim PAN, Li-Zhen
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Pred. No. 1.:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                APPLICANT:
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LOCATION:
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                COUNTRY: United ZIP: 22313-1404
                                                                                                                                       ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAGGGTCCCCGCTCAGCTCCTGGGGCTCCTTCTGCTCTGGCTCCCAGGTGCCAGATGT
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                                                                                                         Alexandria
                                                                        Virginia
: United States
                                                                                                                         E: Burns, Doane,
P.O. Box 1404
                                                                                                                                                          WALSH, Edward E.
HEARD, Cheryl Janne
NEWMAN, Roland Anthony
AVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
AVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
AVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE TH
SEQUENCES: 19
                                                                                                                                                                                                                                                                            CHAMAT, Soulaima
PAN, Li-Zhen
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                                                                                                                                                                                                                                                                                                          Peter
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87.4%;
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                                                                                                                                         Swecker
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                                                                                                                                                                                                                                                                                            Salim
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                         Mathis
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                                                                                                                                                                                     THEREOF
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Sequence 16, Application Patent No. 6200804 GENERAL INFORMATION:

US/09335697B

APPLICANT: BRAMS, Peter

CHAMAT,

Soulaima

TITLE OF

INVENTION:

HIGH AFFINITY

HUMAN

PAN, Li-Zhen
WALSH, Edward E.
HEARD, Cheryl Janne
NEWMAN, Roland Anthony
INVENTION: NEUTRALIZING H:

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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEPAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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hes 333;
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                61 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTCGGAGACAGAGTCACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                   GGGACCAAGGTGGAAATCAAA 381
                                                                      GGGACCAAGGTGGAAATCAAA 387
                                                                                                                                GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA
                                                                                                                                                                       GGAAAAGCTCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246
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                                                                                                                 GAAGATTTTGCAACTTACTATTGTCAACAGGCTTACAGTACCCCCTGGACTTTCGGCCCA
                                                                                                                                                                                                     AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT
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Similarity 87.4%;
33; Conservative
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Pred. No. 1.
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Query Match
Best Local Similarity 87.4
Matches 333; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/335,697B
FILING DATE: 06-Jul-2000
CLASSIFICATION: CURROWN>
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FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        GGAAAGCCCCTAAGCTCCTGATATATGCTGGATCCAATTTGCACCGTGGGGTCCCGTCA
                                                                                                                                                                                                                                                                                 ATCACTTGCCGGGCAGGTCAGAGGATTGCTAGTTATTTAAATTGGTATCAGCACAAACCA
                                                                                                                                                                                                                                                                                                                                                                            GACATCCAGATGACCCAGTCTCCCATCTTCCCCTGTCTGCATCTGTAGGGGACAGAGTCACC
GGGACCAAGGTGGAAATCAAA 387
                                                         GAAGATTTTGCAACTTACTATTGTCAACAGGCTTACAGTACCCCCTGGACTTTCGGCCCA
                                                                             GAAGATTTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCGGCCAA 366
                                                                                                                                                            AGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCCT
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                                                                                                                                                                                                                                                                                                                                                          GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTCGGAGACAGAGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGAGACCCCTGCTCAGCTCCTGGGGCTCCTGCTACTCTGGCTCCGAGGTGCCAGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 705 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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APPLICATION NUMBER:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lonberg,
APPLICANT: Kay, Robe
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US UB/UPU//-
APPLICATION NUMBER: US UB/UPU//-
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/155,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 10-OCT-
                                                                                                                                          PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
US 08/544,404
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APPLICATION NUMBER:
FILING DATE: 03-DEC-
PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 18-MAR-
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MEDIUM TYPE: Floppy disk
                                                                                                          PRIOR APPLICATION DATA:
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                                                                                          APPLICATION NUMBER:
                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                APPLICATION NUMBER: US 0 FILING DATE: 09-MAR-1994
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 10-DE
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 18-NOV
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San
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                                                                                                                                                                                                                                                                                                    UMBER: US 08/165,699
10-DEC-1993
                                                                         JMBER: US 08/728,463
10-OCT-1996
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                                   WO PCT/US96/16433
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FILING DATE: 02-DEC-1996

PRIOR APPLICATION NUMBER: WO PCT/US97/21803

FILING DATE: 01-DEC-1997

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 014643-009040US

PREFERENCE/DOCKET NUMBER: 014643-009040US

TELECOMMUNICATION INFORMATION:
TELEPAN: (415) 576-0200

TELEFAX: (415) 576-0200

TELEFAX: (415) 576-0200

INFORMATION FOR SEQ ID NO: 420:
SEQUENCE CHARACTERISTICS:
LENOTH: 420 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA

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Search completed: September 23, 2002, 18:00:53 Job time: 3224 sec
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      AAGGTTCAGCGGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGCAGCC
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      AAGGTTCAGCGGAAGTGGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCC
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Gapop 10.0 , Gapext 1.0
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411
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(without alignments)
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## ALIGNMENTS

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Human Ig rearranged g
clone S1P15).
L06912
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 405)

Bridges,S.L. Jr., Lee,S.K., Koopman,W.J. and Schroeder,H.W. Jr. Analysis of immunoglobulin gamma heavy chain expression in synovial tissue of a patient with rheumatoid arthritis theum. 36 (5), 631-641 (1993)
                                                                                                                                                                                            Homo sapiens
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                   Location/Qualifiers
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/organism="Homo sapiens"
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gamma-chain
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                                                                           M18513.1 GI:185539

C-region; D-region; J-region; V-region; immunoglobulin heavy chain; immunoglobulin mu-chain; processed gene; variable region subgroup
                                                                                                                                437 bp mRNA linear Human (fetal) rearranged IgM chain VDJ-region mRNA, M18513
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 437)
                                            Homo sapiens
                                                          Homo sapiens foetus liver cDNA to
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NSLRAEDTAIYYCARGVETAAYWGQGTLVTVSS"
58...405
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/note="G00-128-528;
98 c 124 g
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/protein_id="AAA52798.1"
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/tissue_type="Synovium"
/dev_stage="Adult"
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/map="14q32.33"
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83.5%; Pred. No. 8.9e-68;
tive 0; Mismatches 62
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90 a 103 c 142
Chromosome 14q32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Draft entry and computer-readable sequence [1] kindly Schroeder 08-NOV-1988.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="IGH@"
371. .372
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RLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSK
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<1. .>437
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/dev_stage="foetus"
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/gene≖"IGH@"
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TITLE
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Best Local :
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                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                1 ATGGAGTTTTGGGCTGAGCTGGTTTTCCTTGTTCCTCTTTTTGAAAGGTGTCCCAGTGTGAG
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                                                    GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACATGG
                                                                                           TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG
                                                                                                                                                                                                   ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTGCTATTTTAGAAGGTGTCCAGTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 415)
Millil,M., Schiff,C., Fougereau,M. and Tonnelle,C. The VDJ repertoire expressed in human preB cells reselection of bona fide heavy chains Eur. J. Immunol. 26 (1), 63-69 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X81725.1 GI:1212930 diversity region; immunoglobulin heavy chain; variable region; VH-3 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE Related sequences: X65741, X65883 to X65920.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.sapiens rearranged VDJ
X81725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tonnelle,C.
Direct Submission
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                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                       91
                                                                                                                                                                                                                                                                                                                                                                /product="immunoglobulin heavy 373. .415
                                                                                                                                                                                                                                                                                                                                                                                           /product="immunoglobulin heavy 346. .372
                                                                                                                                                                                                                                                                                                                                     /product="immunoglobulin heavy 99 c 122 g 103 t
                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="bone marrow"
/cell_type="pre B-lymphocytes"
/clone_lib="BEL"
/clone="BEL 20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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82.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                     345
                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                     Score 279.4; DB 9;
Pred. No. 5.7e-65;
0; Mismatches 56;
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(BEL20).
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COMMENT
FEATURES
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MEDLINE
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JOURNAL
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Best Local Similarity
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V_region
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                                                                                                   ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTTTATTACTGTCAAACCTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTG
                                             GTGCAGCTGGTGGAGTCTGGGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG
                              GTGCAGCTGTTGGAGTCTGGGGGGGGGCTTGGTACAGCCTGGGGGGGTCCCTGAGACTCTCC
                                                                                    ATGGAGTTTGGGCTGAGCTGGCTTTTTCTTGTGGCTATTTTAAAAAGGTGTCCAGTGTGAG
                                                                                                                                             346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 411)
Millil,M., Schiff,C., Fougereau,M. and Tonn
The VDJ repertoire expressed in human preB
selection of bona fide heavy chains
Eur. J. Immunol. 26 (1), 63-69 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE Related sequences: X65741, X65883 to X65920.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 411)
Tonnelle,C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diversity region; immunoglobulin variable region; VH-3 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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                                                                                                                                           Conservative
                                                                                                                                                                                                                                 ω
                                                                                                                                                                                                                                                            /product="immunoglobulin heavy chain D 363. .411
                                                                                                                                                                                                                                                                                         /product="immunoglobulin heavy chain V region" 353. .362
                                                                                                                                                                                                                                                                                                                                                              /tissue_type="bone marrow"
/cell_type="pre B-lymphocyt
/clone_lib="BEL"
                                                                                                                                                                                                                               /product="immunoglobulin heavy chain J segment"
103 c 127 g 98 t
                                                                                                                                                                                                                                                                                                                                                  /clone="BEL
                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                            rearranged'
                                                                                                                                                          67.8%;
83.0%;
                                                                                                                                                                                                                                                                                                                                                   28"
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                                                                                                                                             0;
                                                                                                                                          Score 278.6; DB 9;
Pred. No. 9.5e-65;
0; Mismatches 59;
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(BEL28).
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BASE COUNT
ORIGIN
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AUTHORS
TITLE
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AUTHORS
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KEYWORDS
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                                            Query Match
Best Local S
Matches 349
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                                              Local Similarity
mes 349; Conserv
AACTGGTTCAACTGGTTCGACCCCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCTTGACTACAGGGTCTGACTCCTGGGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTCCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATAC
                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eurocate (17)

1 (bases 1 to 417)

Milili,M., Schiff,C., Fougereau,M. and Tonnelle,C.

The VDJ repertoire expressed in human preB cells reserved to the control of bona fide heavy chains selection of bona fide heavy chains

Selection of bona fide heavy (1996)
                                                                                                                                                                                                                                                                                                      Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immur Marseille-Luminy, Case 906, 13288 Marseille, Cedex Related sequences: x65741, x65883 to x65920.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diversity region; immu variable region; VH-3
                                                                                                                                                                                                                                                                                                                                         Direct Submission
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X81729
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 417)
                                                                                                              92
                                              Conservative
                                                                                                              ۵
                                                                                                                                /product="immunoglobulin heavy 375. .417
                                                                                                           /product="immunoglobulin heavy 94 c 127 g 104 t
                                                                                                                                                      /product="immunoglobulin 353. .374
                                                                                                                                                                                               /tissue_type="bone marrow"
/cell_type="pre B-lymphocytes"
/clone_lib="BEL"
/clone="BEL 34"
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                           /rearranged
                                                                                                                                                                                                                                                      /chromosome="14"
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                                                       67.5%;
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/H-3 family.
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                                             0
                                          Score 277.4; DB Pred. No. 2e-64; 0; Mismatches
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region
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(BEL34).
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                                                                Length 417;
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Wang, X. and Stollar, B.D.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (30-APR-1998)
School of Medicine, 136
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AF062285
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Homo sapiens clone Xu-57
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/codon_start=1
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/product="immunoglobulin heavy chain variable region"
/product="immunoglobulin heavy chain variable region"
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/db_xref="GI:3171043"
/translation="MELGLCWVFLVAILEGVQCEVQLVESGGGLVQPGGSLRLSCAAS
GFTESSYEMMAVRQAPEKSLEMVSYISSSGSTIYYADSVKGRETISRDNAKNSLYLQM
NSLRAEDTAVYYCARDFSSSWYYEGDYWGQGTLVTVSSG"
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1 to 423)
                                                                                                                                                                                                                                                                                                      /chromosome="14"
/map="14q32.33"
                                                                                                                                          /gene="IGH"
                                                                                                                                                                                                                      /cell_type="peripheral B lymphocyte"
/tissue_type="blood"
/note="from young repertoire Xu"
                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                            2 (bases 1 to 402)
Wang, X. and Stollar, B.D.
Direct Submission
Submitted (24-ApR-1998) B
School of Medicine, 136 H
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Primates;
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1 (bases 1 to 402)
Wang, X. and Stollar, B.D.
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/gene="IGH"
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/organism⇒"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
                                     Location/Qualifiers
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                                                            (24-APR-1998) Biochemistry Department, Tufts U Medicine, 136 Harrison Ave., Boston, MA 02111,
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82.2%;
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A 02111, USA
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                                         Eukaryota; Metazoa; Chordata; Craniata; Verrebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
1 (bases 1 to 411)
Noppe,S.M., Heirman,C., Bakkus,M.H., Brissinck,J.,
                                                                                                                           Homo sapiens mRNA for Ig
AJ234277
AJ234277.1 GI:3821217
heavy chain; immunoglobul
The genetic variability of the VH genes in impact of the hypermutation mechanism
                              Thielemans, K.
                                                                                                Homo sapiens
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58. .>402
/gene="IGH"
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GFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSKNTLYLOM
NSLRAEDTAVYYCAKDGGVYWGQGTLVTVSSG"
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/clone="Xu-15"
/cell_type="peripheral B lymphocyte"
/tissue_type="blood"
/note="from young repertoire Xu"
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/product="immunoglobulin heavy chain variable region"
/protein_id="AAC18296.1"
/db_xref="GI:3170987"
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5.4e-64;
hes 57;
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n variable region,
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n, clone C6/7.
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Direct Sub
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                  Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 113)
                                                                                       Z47226.1 GI:1197316
                                                                                                                           H.sapiens mRNA
Theze,J.
         Demaison,C.,
                                                       Homo sapiens
                                                                                                                                       HSVHIC10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-OCT-1998) Noppe S.M., Laboratory of Physiology, Free University of Brussels Laarbeeklaan 103/E, 1090 Brussels, BELGIUM
                                                                   human
                                                                              immunoglobulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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<1. .>411
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100 c 12
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/clone="C6/7"
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/isolate="follicular lymphoma
/db_xref="taxon:9606"
/chromosome="14"
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         David, D.,
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82.5%;
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                                                                            immunoglobulin
                               Chordata;
Primates;
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        Letourneur, F.,
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                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                           heavy
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        Zouali, M.,
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KEYWORDS

D-region; J-region;

V-region;

immunoglobulin heavy

chain;

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VERSION ACCESSION DEFINITION

M34024.1 partial cds. M34024 Human

GI:185267

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                                                                                                                                                                                                                                                                                                                                                                                                                              342;
              HUMIGHCXE
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Submitted (16-DEC-1994) Christophe Dem
d'Immunogenetique Cellulaire-institut
Roux, Paris, 75015, FRANCE
3 (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A cDNA/anchor-PCR approach to analyse the human VH gene repertoire expressed by peripheral CD19+ B cells reveals a strong blas usage unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 82.0
42; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="immunoglobulin variable 101 c 129 g 95 t
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/cell_type="B-lymphocyte"
1..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="CDN3IC10"
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Pred. No. 7.9e-64;
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 PRI 11-JUL-1995
M43) mRNA,
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TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA----
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                                                                   TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCCAGAGAGAACGCCAACAACACACTG
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Schroeder, H.W. Jr. and Wang, J.Y.
Preferential utilization of conserved immunoglobulin heavy
variable gene segments during human fetal life
Proc. Natl. Acad. Sci. U.S.A. 872 (1691), 6146-6150 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Draft entry and computer-readable sequence for [Proc. Natl. Sci. U.S.A. (1990) In press] kindly submitted by H.W.Schroeder, Jr., 04-MAY-1990.
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liver cDNA to mRNA.
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/protein_id="AAA69729.1"
/db_xref="GCI:567121"
/db_xref="GDB:GOO-118-731"
/translation="GIRCFHLVIRTEORELIMEFGLSWLFLVAILKGVQCEVOLLES
GGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYADSVK
GGRTISRDNSKNTLYLQMNSLRAEDTAVYYCAKKDWNDNWFDPWGQGTLVTVSS"
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/organism="Homo sapiens"
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/tissue_type="liver"
/dev_stage="104 day foetus"
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/isolate="H8409"
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/clone="M43"
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                                                                                                                                                                                                                                                                           1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTCTTTGAAAGGTGTCCAGTGTGAG
                                           ACATGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAAGAACGCCAACAAC
                                                                                                  GCTCCAGGGCAGGGGCTGGAGTGGGTTCTCACGTATTAGTAGTAGTAGTGGTGATCC-----C
                                                                                                                                                             TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG
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 ACACTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG
                            GCATACTACGCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAC
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Submitted (23-OCT-1998) Noppe S.M.,
University of Brussels Laarbeeklaan
Location/Qualifiers
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AJ234278.1 GI:3821218
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Noppe, S.M., Heirman, C.,
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/gene="VopLVDJ"
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/isolate="follicular lymphoma
/db_xref="taxon:9606"
/chromosome="14"
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              GTGCAGCTGGTGGAGTCTGGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120
AGCTTGACTACAGGGTCTGACTCCTGGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                                                              ATGGAGTTTGGGCTGAGCTGGCTTTTTCTTGTGGCTATTTTAAAAAGGTGTCCAGTGTGAG
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Mechanisms that generate human immunoglobulin diversity operate from the 8th week of gestation in fetal liver Eur. J. Immunol. 23 (1), 110-118 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (09-JUN-1992) C. Tonnelle, Centre d'Immunologie Marseille-Luminy, Case 906, 13288 Marseille Cedex 9, FRANCE 2 (bases 1 to 437)
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1 (bases 1 to 437)
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Z14201 x65741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ig D-segment; Ig heavy chain; Ig
variable region; immunoglobulin.
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                                                                                                                               Conservative
                                                                                                                                                                                                                            93
                                                                                                                                                                                                                                                                                                                       /translation="merglismlflvailkgvQCevQLLeSgGgLvHPGGSLRLSCAAS GFTESSYAMSWVRQAPCKGLEWVSAISGSGGSTYYSDSVKGRLTISRDNSKNTLYLQM NSLRAEDTAVYYCARWRDLDYWGQGTLVTVSS"

93...386
                                                                                                                                                                                                                                                         /note="diversity region" 399. .437
                                                                                                                                                                                                                                                                                         /note="variable region"
387. .398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="feral liver"
/clone_lib="E54"
36. .92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="14"
/clone="3.3"
                                                                                                                                                                                                                        /note="joining region"
104 c 136 g
                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA78570.1"
/db_xref="GI:30962"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        (VDJ) "
                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                            66.6%;
82.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .>437
                                                                                                                             0;
                                                                                                                                         Score 273.8; DB 9
Pred. No. 1.9e-63;
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                                                                                                                             Mismatches
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variable region (VDJ).
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                                                                                                                            9;
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LOCUS
                                                                       ORIGIN
                                                                                   BASE COUNT
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Query Match
Best Local Similarity
Matches 348; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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misc_feature
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J. Clin. In
93232287
                                                                                                                                                                                                                                                                                                                                                                    Bone marrow cells in X-linked agammaglobulinemia express pre-B-specific genes (lambda-like and V pre-B) and present immunoglobulin V-D-J gene usage strongly biased to a fetal-like
                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-APR-1992) C. Marseille, Case 906, 13288 2 (bases 1 to 420)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSIGHXX13 420 bp
H.sapiens mRNA for XLA IG heavy
X65895 S58681
X65895.1 GI:395092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; L. (bases 1 to 420)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diversity region;
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  Conservative
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                                                                                                            1. .57

58. .352

/note="variable region"

353. .377

/note="diversity region"

378. .420
                                                                                                                                                                                                                                                                                                                                           Invest. 91 (4), 1616-1629 (1993)
                                                                                  /note="joining region"
99 c 135 g
                                                                                                                                                                                                 /tissue_type="bone marrow"
/cell_type="pre-B"
/clone_lib="LE library"
/clone="LE 3-12"
                                                                                                                                                                                                                                                            /chromosome="]
                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                66.4%;
81.7%;
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Score 272.8; DB 9;
Pred. No. 3.5e-63;
0; Mismatches 57;
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                                                                                      102
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chain VDJ region
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415 TCCTCA 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGAGTTTGGGCTGAGCTGTTTTCCTTGTGGCTATTTTAAAAGGTGTCCAGTGTGAG
                                                                                                                                                                                                                         Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRAI Related sequences: X65741, X65883 to X65920.
                                                                                                                                                                                                                                                                                                             The VDJ repertoire expressed in human preB cells reflects the selection of bona fide heavy chains Eur. J. Immunol. 26 (1), 63-69 (1996)
                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (Dases 1 to 417)
Milili,M., Schiff,C., Fougereau,M. and Tonnelle,C.
                                                                                                                                                                                                                                                                                                                                                                                                                            diversity region; immunoglobulin variable region; VH-3 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.sapiens rearranged VDJ
X81734
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   89
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                          /product="immunoglobulin heavy chain D 376. .417
/product="immunoglobulin heavy 97 c 127 g 104 t
                                                 /product="immunoglobulin heavy
349. .375
                                                                                                 /tissue_type="bone marrow"
/cell_type="pre B-lymphocytes"
/clone_lib="BEL"
/clone="BEL 56"
                                                                                                                                                   /rearranged
                                                                                                                                                             /chromosome="14"
                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                   Direct Submission
Submitted (23-OCT-1998) Noppe S.M.,
University of Brussels Laarbeeklaan
Location/Qualifiers
                                                                                                                                                                                                                                                  Noppe, S.M.
                                                                                                                                                                                                                                                                                                        The genetic variability of the VH genes in impact of the hypermutation mechanism Br. J. Haematol. 107 (3), 625-640 (1999)
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 414)

Noppe, S.M., Heirman, C., Bakkus, M.H., Brissinck, J., Schots, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens mRNA for Ig
AJ234298
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heavy chain; immunoglobulin superfamily;
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                                                                                                                                                                                                                                                                                          20050318
                                                                                                                                                                                                                                                                    (bases 1 to 414)
/dev_stage="adult"
/clone="C4/5/6"
/cell_type="follicular lymphoma"
                                                                               /db_xref="taxon:9606"
/chromosomo-":'
                                                                                                               /organism="Homo sapiens"
/isolate="follicular lym
                                                           /rearranged
                                                                             /chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.3%;
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heavy chain variable region,
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Best Local Similarity 81.9%;
Matches 344; Conservative
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355 GACTATGGTTCGGGGAGATATGACTACTGGGGGGCAGGGAACCCTGGTCACCGTCTCCTCA 414
                                                                                                                                                 61
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                                                                                                                                                                           GTGCAGCTGGTGGAGTCTGGGGGGCGTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120
       ACTACAGGGTC------TGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                                                                                     91
                                                                                                                                                                                                                                                1. 414
/gene="WarLVDJ"
<1. .414
/gene="WarLVDJ"
gene="100 c 130 g
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Pred. No. 4.5e-63;
0; Mismatches 61; Indels 15; Gaps
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Search completed: September 23, 2002, 17:50:15 Job time: 6869 sec

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Minimum DB :
Maximum DB :
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Listing first 45 summaries
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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## ALIGNMENTS

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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MCC clone distribution: MCC clone distribution: MCC clone distribution: MCC clone distribution the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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IMAGE:3054342 5', mrNA sequence.
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//db_xref="taxon:9606"
//db_xref="taxon:9606"
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//clone_lib="NH_MGC_36"
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//cell_line="McC85"
//ab_host="bHl0B (LTI)"
//note="vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
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Homo sapiens cDNA clone
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BM007475.1 GI:16521829
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                     Plate: LLCM1913 row: d column: High quality sequence stop: 608.
                                                                                                            cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5440475"
/clone_lib="NIH_MGC_113"
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Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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                                                                                                      Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution informs

found through the I.M.A.G.E. Consortium/LLNL at:
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AW402613 5050505 Fig. 10 pp. 10
                                           Seq
                                                                          www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Location/Qualifiers
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Pred. No. 1.3e
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collecti
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (I
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1164)
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                                                                                                                                                                                                                                                                          Homo sapiens
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BF974771
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/organism="Homo sapiens"
/db_xref="taxon.9606"
/clone="IMAGE:305305"
/clone_lib="NIH_MCC_36"
/tissue_type="jerminal center B cells"
/cell_type="MGC85"
/cell_line="MGC85"
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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_1: 
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Pred. No. 2.7e-66;
0; Mismatches 58;
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UI-HF-BKO-aag-a-05-0-UI.rl NIH_MGC_36
IMAGE:3054608 5', mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NH_MGC Library."
84 a 313 c 330 g 236 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:4336541"
/clone_lib="NIH_MGC_48"
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National Institutes of Health, Mammalian Gene Collection (MGC)

LUnpublished (1999)

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/db_xref="taxon:9606"
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/tissue_type="1ymph"
/cell_type="germinal center B content of the content of 
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/note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
a 110 c 137 g 103 t
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Pred. No. 8.2e-66;
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                                                                                 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCG------
                                                                                                                                            GTGCAGCTGGTGGAGTCTGGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG
                                                              TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCC
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                               ------AGCTTGACTACAGGGTCTGACTCCTGGGGCCCAGGGAGTCCTGGTCACCGTC 405
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Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

DNA Sequencing by: M.B. Soares Lab

Clone distribution: MGC clone distribution information

found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (1999)
Contact: Robert Strausberg, Ph.D.
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Seq primer: M13 Forward.
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AW403220
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a 127 c 143 g 103 t
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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco
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/clone="IMAGE:3055710"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
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/cell_line="MGC85"
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                                                   GCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
                                                                                                                                  TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
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                                 GCTCCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTAGTACCATATAC
                                                                                                  TGTGCAGCCTCTG-----GATTCACCTTCAGTAGTTATGGAATGAACTGGGTCCGCCAG
                                                                                                                                                                                                                                                                                                         318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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AW403059.1 GI:6921885
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UI-HF-BKO-aai-f-10-0-UI.rl NIH_MGC_36 H
IMAGE:3054090 5', mRNA sequence.
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Seg primer: M13 Forward.
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                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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/cell_line="MGC85"
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/tissue_type="lymph"
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Pred. No. 4.9e-64;
0; Mismatches 55
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                                                                     TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
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TGTGCAGCCTCTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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UI-HF-BKO-aau-h-03-0-UI.rl NIH_MGC_36
IMAGE::055324 5', mRNA sequence.
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                             /lab_host="DHIOB (LTI)"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Lou
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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/tissue_type="lymph"
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/cell_line="MGC85"
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/clone="IMAGE:3055324"
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-GATTCACCTTCAGTGATTATGAATTGAACTGGGTCCGCCAG
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                                                                                                                                                                                                                     Score 269; DB 9;
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                                  ATGGAACTGGGGCTCCGCTGGGTTTTCCTTGTTGCTATTTTAGAAGGTGTCCAGTGTGAG 84
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                                                                                                           343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
clone distribution: MGC clone distribution informs
found through the I.M.A.G.E. Consortium/LLNL at:
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Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, M
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Seq primer: M13 Forward.
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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Low
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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/clone="IMAGE:3053139"
/clone_lib="NIH_MGC_36"
/tissue_type="lymph"
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/cell_line="MGC85"
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UI-HF-BK0-abj-e-10-0-UI.rl NIH_MGC_36 Homo
IMAGE:3056371 5', mRNA sequence.
AW408304
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Seg primer: M13 Forward.
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/Cell_line="MGCD3"
//Lab_host="DH10B (LTI)"
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//Lab_host="Nector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
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                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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/note-"Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/note-"Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
115 c 143 g 120 t
                                                                                                                      /clone_lib="NIH_MGC_36"
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/cell_type="germinal center B
/cell_line="MGC85"
                                                                                                                                                                                            /clone="IMAGE:3056926"
                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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.. Staudt, ...

-1do, Ph.D. au

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_36 Homo sapiens
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BG757947
                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D.,
                                                                                                                                                                                                                                                                                           http://image.llnl.gov
Plate: LLCM1703 row:
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      numan.
                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Ling Hong/Rubin Laborator cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                     e: LLCM1703 row: f column: quality sequence stop: 736.
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/clone_lib="NIH_MGC_48"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="PH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: xhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Li
Hong in the laboratory of Gerald M. Rubin (University of
                                                                                                                                                                        /db_xref="taxon:9606"
/clone="IMAGE:4854932"
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                /organism="Homo sapiens"
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86.2%;
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                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 741)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (199)
Contact: Robert Strausberg, Ph.D.
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BG754024.1
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602709552F1 NIH_MGC_48
                                                                                                                                                                             found Introduction 14 http://image.llnl.gov
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plate: LLCW1686 row: g column: 14
plate: -'''the segmence stop: 735.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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07; Conservative
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/tissue_type="primary B-cells from tonsils (cell line)"
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/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note="Organ: CDNA made by oligo-dT priming.
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203 c 206 g 165 t
                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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86.2%;
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Pred. No. 6.5e-63;
0; Mismatches 43
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                  Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence
CONA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution informs
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW403707 510 bp mRNA UI-HF-BK0-abh-f-08-0-UI.rl NIH_MGC_36 Homo mAGE:3056391 5', mRNA sequence.
                                                                                                     Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
/clone="IMAGE:3056391"
/clone_lib="NIH_MGC_36"
                                                  /organism="Homo sapiens"
                                                                                       Location/Qualifiers
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              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1618 row: f column: 18
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 908)
                                                                                                                                                                                                                                                                                                                                                                                        mRNA sequence.
BG686881
BG686881.1 GI:13918278
EST.
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National Institutes of Health, Mammalian
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602650867F1 NIH_MGC_48 Homo sapiens
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/cell_type="germinal center B cells"
/cell_line="MGC85"
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/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
  sequence stop:
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Pred. No. 1.1e-62;
0; Mismatches 78;
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Matches
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GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACATGG
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                                                                                                                                                                                                                                                                                                                                         GTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
                                                                              TACGCAGACTCAGTGAAGGGCCGATTCACCATCTCCAGAGACACGCCAAGAACTCACTG
                                                                                                                       TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG
                                                                                                                                                                                                                                        TGTGCAGCCTCTG----
                                                                                                                                                                                                                                                                             TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
                                                                                                                                                            GCTCCANGGAAGGGGCTGGAGTGGGTCTCATCCATTAGTAGTAGTAGTAGTACATATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="primary B-cells from tonsils (cell line)"
/lab host="DH10B (phage-resistant)"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
/note="Organ: Sites using the following 5' adaptor: GGCACGAGG). Size=selected >500bp
/for average insert size 1.8kb. Library constructed by Ling
/Hong in the laboratory of Gerald M. Rubin (University of
/California, Berkeley) using ZAP-cDNA synthesis kit
/Stratagene) and Superscript II RT (Life Technologies).
/note: this is a NIH_MGC Library."
/note: this is a NIH_MGC Library."
/note: Vector and Superscript II RT (Life Technologies)
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/clone="IMAGE:4763153"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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85.2%;
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Pred. No. 4.1e-62;
0; Mismatches 47;
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Search completed: September Job time: 4520 sec 23, 2002, 17:07:01

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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  369.4
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SIDS1/gcgdata/geneseq/geneseqn-emb1/Wa198.DAT:*

SIDS1/gcgdata/geneseq/geneseqn-emb1/Wa198.DAT:*

SIDS1/gcgdata/geneseq/geneseqn-emb1/Wa198.DAT:*

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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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Compugen Ltd
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Traget plasmid Man
Human coding seque
Human cDNA encodin
Human cDNA encodin
                                                                                                                                                                                          Description
Human antibody hea DNA seq ID No: 58. Nucleotide sequenc
                                                          Chimeric antibody
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247.6	250.6	50.	251.2	51.	51.	51.	252	UT	252.2	252.2	252.6	252.6	253.2	253.2	254.6	254.6	254.6	254.6	256.6	256.8	258	258	258.2	259.6	260	261	261.2	261.6	262.2	266	67	67	7	267.4	
60.2	61.0	1.	61.1	1.	61.3	1.	61.3	61.3	61.4	61.4		1		_	٢	۲.	Ξ.	61.9	2.	2	2	2	2	63.2	ω.	ω.	ω.	ω	w	64.7	5	65.1		65.1	65.1
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AAS62797	AAQ64051	AAH18432	AAX01214	AAZ22787	AAQ64065	AAQ31888	AAD07360	AAA15694	AAT85839	AAT46130	AAA46896	AAA46870	AAA46894	AAA46866	AAA46891	AAA46892	AAA46890	AAA46864	AAT72237	AAS91077 ·	AAV41432	AAV41429	AAQ71717	AAV41431	AAS22532	AAQ03610	AAH98760	AAS22531	AAH98583	AAS22625	AAF69242	AAF69186	AAF69130	AAH76645	AAH74285
cDNA sequence #584	Sequence of the VH	Human cDNA sequenc	Human antiFc epsil	Human anti-ganglio	Anti-cancer monocl	CLN-IgG gamma. Sy	Human DNA encoding	Cancer suppressor	Monoclonal antibod	Monoclonal antibod	DNA encoding the h	DNA encoding the h	DNA encoding the h		DNA encoding the h	DNA encoding the h	cDNA encoding the	DNA encoding the h	Humanised reshaped	DNA encoding novel	Plasmid Hu19DHcpcd	Plasmid Hu19BHcpcd	Monoclonal antibod	Plasmid Hu19CHcpcd	Human cDNA encodin	Sequence encoding		Human cDNA encodin	Human EST-derived	Human cDNA encodin	H	Human antibody H c	Human antibody H c	Humanised anti-PTH	Nucleotide sequenc

## ALIGNMENTS

RESULT AAV33310

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AAV33310 standard; DNA; 411 BP

AAV33310;

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misc_feature
                                                                                                                                                    CDS
                                                                                                                                                                                                         Anti-human CD23 5E8 monoclonal antibody; heavy chain variable region; human CD23; IgE; FceRii/CD23; gamma-1 constant region; palma-3 constant region; allergy; inflammation; autoimmune disease; allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia; ss.
                                            misc_feature
                                                                 mat_peptide
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                                                                                                                                                                                                                                                                   Anti-human CD23 5E8 moclonal antibody heavy chain variable region DNA
                                                                                                                                                                                                                                                                                           18-NOV-1998 (first entry)
                                                                /note= "CDS c
1..57
/*tag= b
58..411
                                            /*tag= c
148..168
        /*tag= d
/note= "encodes CDR 1 region"
211..261
                                                                                                                                                            Location/Qualifiers
                                                                                                                          /*tag= a
/product= "anti-human CD23 5E8 heavy chain variable
                                                                                                                                     /*tag=
                                                       C
                                                                                                              region"
                                                                                                    does not contain a stop codon'
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New anti-human CD23 monoclonal expression to treat or prevent
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20-FEB-1997;
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Local Similarity
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                                                                                                                                                                        GTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCCTGAGACTCTGG
a&tacagggtctgactcctggggccagggagtcctggtcaccgtctcctca
                      ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                                                                                                           TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG
                                                                                                                                                                                                                                                                 gctccagggcaggggctggagtgggtctcacgtattagtagtagtggtgatcccacatgg
                                                                                                                                                                                                                                                                                          GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTAGTGGTGATCCCACATGG
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Rhesus macaque
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This is the nucleotide sequence of novel target plasmid Mandy.

The plasmid includes an inactivated murine dihydrofolate reductase

(DHER) gene, the Escherichia coil beta galactosidase gene,

baculovirus DNA, a cassette comprising the promoter and enhancer

elements from cytomegalovirus and SV40 virus, the E. coli

beta-glucuronidase (GUS) gene, firefly luciferase gene, an

inactivated Salmonella typhimurium histidinol dehydrogenase (HisD)

gene and transposon Tn5 neomycin phosphotransferase (neo) gene

sequences, in a pRR-derived backbone, and also an anti-human CD23

IgE receptor human gamma-1 monoclonal antibody 5EB gene. The

invention provides a novel method for integrating a desired

exoqueous DNA at a target site within the genome of a mammallan

cell with a 'marker plasmid' such as Desmond (see AAV61792), which

contains a unique sequence that is foreign to the mammalian cell

genome and which provides a substrate for homologous recombination,

followed by transfection with a 'target plasmid', such as Mandy

con Molly (see AAV61793), containing a sequence which provides for

homologous recombination with the unique sequences contained in

the marker plasmid, and further comprising a desired DNA that is

con municulated those the mammalian cells, typically an

immunoglobulin or other secreted mammalian and system utilises the neo gene as a

dominant selectable marker. The neo gene is split into 3 the mammalian cells.

Exon 3 is present on the marker plasmid

into the mammalian cells. Exons I and 2 are present on the

conteins and and and are and and are and a present on the

conteins the mammalian cells. Exons I and 2 are present on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      turgeting plasmid, and are separated by an intron into which at least one gene of interest is cloned. Homologous recombination of the targeting vector with the integrated marking vector results in correct splicing of all 3 exons of the neo gene and expression of a functional neo protein. The method is applicable to all mammalian cells, and can be used to express any type of recombinant protein. The use of a triply spliced selectable marker means that all selected colonies arise from homologous recombination. In addition, the number of colonies that need to be screened to identify high producer clones is reduced. An amplifiable gene can be inserted on integration of the marking vector, so that when a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene is targeted to this site, the gene is further enhanced by gene amplification.
                       e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19035 BP; 4705 A; 4968 C; 4822 G; 4519 T; 21 other;
                       Site specific integration of DNA in mammals for expressing,
                                                     immunoglobulins - comprises homologous recombination using
                                                                             selectable marker and target plasmids.
                                                                                                                                        Example 1; Fig 10; 114pp; English.
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GTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120 121 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180 Gaps 1 ATGGAGTITGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTGAAAGGTGTCCAGTGTGAG 60 89.9%; Score 369.4; DB 19; Length 19035; 93.7%; Pred. No. 2e-94; 1ve 0; Mismatches 26; Indels 0; Best_Local Similarity 93.7 Matches 385; Conservative Query Match 61 ŏ δ g g δ

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getecagggcaggggctggagtgggtctcacgtattagtagtagtggtgatcccacatgg 9671 240 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 181 9612 g ò

9552 tgcgcagcctccgggttcaggttcaccttcaataactactacatggactgggtccgccag

TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300 241 ò

TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG

gctccaggggaaggggctggagtgggtctcatccattagtagtagtagtagttacatatac

GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG

TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG BP.

(first entry)

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241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACAGTG
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                                                                                                                                                                                                                361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
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                                                                                                                                                                                                                                                                              Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis; Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy; signal transduction inhibition; tissue fibrosis; atherosclerosis; ds.
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                         9672 tacgcagactccgtgaagggcagattcaccatctccagagagaacgccaagaacacctg
                                                                                          411
                                                                             ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating TGF-beta associated s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 12; Page 94-95; 118pp; Japanese.
                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                       Human coding sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human monoclonal antibodies
useful for treating תמד-אבר
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immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiaviral; antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to
                                                                                                                    ss; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                            Human cDNA encoding a novel human protein #99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 306-308; 894pp; English.
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Indels

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Length 458;

Score 293; DB 22; Pred. No. 2.7e-73; 0; Mismatches

71.3%; 83.9%;

al Similarity 83.9 345; Conservative

Query Match

Best Local Matches 34

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61 GTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120

Isolated polypeptides useful for treating anti-inflammatory diseases,

Drmanac RT

Liu C,

Tang YT,

(HYSE-) HYSEQ INC

WPI; 2001-451939/48.

P-PSDB; AAU14225

25-JAN-2001; 2001WO-US02623 25-JAN-2000; 2000US-0491404 nervous system disorders, and for reqenerating bone and cartilage

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                 protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting contraceptive, treating osteoporosis and osteoarthritis, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia. Alzhelmer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunomodulatory; cytostatic; neuroprotective; vulnesary; nootropic;
anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
antibacterial; antiallerquic; dermactological; haemostatic; antiasthmatic;
thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   360
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raise antibodies/elicit an immune response, to determine quantitative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gotoccagggaaggggotggagtgggtctcatctattagtggtagttcgggtaccacatac 395
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                                                                                                                                                                                fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ATGGAGTTTGGGCTGAGCTGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG
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                                                                                                                                                                                                                                                                                                                                                    DB 22; Length 1710;
                                                                                                                                                                                                                                                                                                                                   Score 282.6; DB 22; Leuge...
Pred. No. 3.6e-70;
.....trhes 64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 407
                                                                                                                                                                                                                                                                                      Sequence 1710 BP; 401 A; 464 C; 409 G; 436 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human cDNA encoding a novel human protein #96.
                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  Query Match 68.8%;
Best Local Similarity 82.8%;
Matches 337; Conservative
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proteins or their active domains. The polypeptides, polynucleotides and proteins or their active domains. The polypeptides, polynucleotides and antibodies railsed against the polypeptides are used in a method of cantibodies railsed against the polypeptides are used in a method by the aberrant protein expression or activity. The polypeptides can be used as complexely are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and production of recombinant proteins, and in antibody anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, independent and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection.
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0; Mismatches
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82.8%;
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Best Local Similarity 82.8°
Matches 337; Conservative
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Best Local
Matches 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New antibodies have been developed which are specific for human parathormone related peptides (hPTRP). The antibodies comprise chimeric L and/or H chains, where the C region is of human and L region of mouse, origin. The present sequence encodes a specifically claimed region of an antibody of the invention. Host cells, transformed with vectors containing DNA encoding antibodies of the invention, can be used to produce the antibodies. The antibodies may be used to treat hypercalcaemia, especially that due to a malignancy, e.g. cancers of pancreas, lung, throat, larynx, tongue, qum, ososphagus; stomach, liver, breast, kidney, bladder, womb or prostate or malignant lymphoma. They may also be used for treatment of hypophosphaemia such as that due to
                                                                                                                                                                                                      Chimeric; antibody; human parathormone related peptide; hPTRP; mouse; L chain; H chain; hypercalcaemia; cancer; malignant lymphoma; CDR; hypophosphaemia; pathogen; vitamin D resistance; V region; C region; humanised; ds.
                                                                                                                                                                               Chimeric antibody fragment against hPTRP encoding cDNA SEQ ID NO:58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New chimeric antibodies against human parathormone related peptide(s) - useful for, e.g. treatment of hypercalcaemia and other disorders caused by malignant neoplasm(s)
          361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 407
                         T; 0 other;
                                                                                                                                                                                                                                                                                                                                       1..411
/*tag- a
/note- "no stop codon given"
1..57
/*tag- b
58..411
/*tag- c
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                                                                                                    AAV24243 standard; cDNA to mRNA; 411 BP
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96JP-0255196
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Chimeric - Homo sa
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                                                                                                                                                                                                                                                                     Synthetic.
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65.1%; Score 267.4; DB 19; Length 411;

Query Match

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                                                                                                                                                   GCTCCAGGGCCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
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                                                             9
              Gaps
                                     ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; parathyroid hormone related protein; PTHrP; cachexia; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibitors of binding of parathyroid hormone related peptide to its receptor - useful for, e.g. treatment of cachexia arising from cancer or other diseases
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 Pred. No. 4.5e+66;
0; Mismatches 66;
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ID AAX00116 standard; cDNA to
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 al Similarity 81.3
339; Conservative
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/note=
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P-PSDB; AAW89635.
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15-MAY-1997;
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(CHUS ) CHUGAI SEIYAKU
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                 cachexia containing a substance which inhibits the binding of a parathyroid hormone related peptide (PTHFP) to its receptor, as an active component. This substance may be an antagonist to the receptor, or an antibody (preferably monoclonal) or antibody fragment, recognising PTHFP. The antibody is preferably humanised or chimeric. The present invention also describes a humanised antibody prepared by hybridoma 2.57-137-1 (FERM BP-561). The composition is used for the treatment of cachexia arising in connection with diseases such as cancer, thereby improving the quality of life of the patient. The present sequence encodes a human antibody heavy chain from the present
                                                                                                                                                                                                                                                                               180
                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                         301 TITCTICAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGICIAITACIGIGCGAGCTIG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 atggggtttggggctgagctgggttttcctcgttgctcttttaagaggtgtccagtgtcag
                                                                                                                                                                                                                                                                                                             TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG
                                                                                                                                                                                                                                                                                                                                                       GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG
                                                                                                                                                                                                                                                                                                                                                                             getecaggeaaggggetggagtgggtggcaaccattagtagtggtggtagttacacctac
                                                                                                                                                                                                                                                                                                                                                                                                                                                               tatctgcaaatgaacagcctgagagctgaggacacggctgtgtattactgtgcgagacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parathyroid hormone related peptide; PTHrP;
                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                              DB 20; Length 411;
                                                                                                                                                                                                     Indels
           for the
                                                                                                                                               Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
                                                                                                                                                                               Score 267.4; DB 20;
Pred. No. 4.5e-66;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                              65.1%;
ilarity 81.3%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
          present invention
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                                                                                                                                                                              Query Match
Best Local Similarity
Matches 339; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq ID No: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200000219-A1
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                                                                                                                             invention.
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A composition for the treatment of hypercalcemic crisis contains as active component a substance which inhibits the binding of parathyroid hormone related peptide (PTHIP) to its receptor. The inhibitor is used for the treatment of hypercalcemic crisis, such as that associated with
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                                                                                                                 Treatment of hypercalcemic crisis with a substance inhibiting binding of parathyroid hormone related peptide to its receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TITICTICAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGICIATIACIGIGCGAGCIIG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            235 tatccagacagtgtgaaggggcgattcaccatctccagagacaattccaagaacacgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 267.4; DB 2:
Pred. No. 4.5e-66;
0; Mismatches 66
                                                                                                                                                                                              Example 4; Page 98-99; 120pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of a human protein.
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81.3%;
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Matches 339; Conservative
Tsunenari T;
                                           WPI; 2000-117115/10.
P-PSDB; AAY77514.
                                                                                                                                                                                                                                                                                                                                                                         malignant tumour.
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                                                                                                                                                                                                                                                                                                                                                                                      The specification describes a tissue decomposition inhibitor, which comprises a substance that inhibits peptides associated with parathyroid hormone (PTH) from binding with their receptor. The method is used to inhibit tissue decomposition caused by cancer cachexia, septicemia, heavy external injury or muscular dystrophy, and for treating patients with elevated cytokine (Interleukin-6, Granulocyte Colony stimulating factor, Interleukin-11 and Leukemia inhibitory factor) levels. It may also be used for preventing weight loss caused by cancer cachexia. The present sequence encodes a protein, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue decomposition inhibitor that prevents parathyroid hormone associated proteins from binding to its receptor \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 267.4; DB 2 Pred. No. 4.5e-66;
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                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 107-108; 132pp; Japanese.
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                                                                                                                                                                                                                                                 Onuma
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81.3%;
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1..411
/*tag=
1..57
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58..411
/*tag=
                                                                                                                                                                                                                   (CHUS ) CHUGAI SEIYAKU
                                                                                                                                                                                                                                               Saito H, Tsunenari T,
                                                                                                                                                                                                                                                                          WPI; 2001-550131/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 339; Conserv
                                                                                                                                                                                                                                                                                         P-PSDB; AAG67112
                                                                                                 WO200164249-A1
                                                                                                                             07-SEP-2001
                            sig_peptide
                                                        mat_peptide
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Best Local Si
Matches 339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parathyroid hormone-associated peptide binding inhibitors useful for treating dental disease
                                                                                                                                                         SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification describes a treatment for dental diseases. The treatment comprises a substance that inhibits binding between parathyroid hormone-associated peptide and its receptor. The present sequence encodes a human protein, which is used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parathyroid hormone-associated peptide; PTHrP; dental disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 411;
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/*tag= a
/note= "no termination codon given"
58..411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 267.4; DB 22;
Pred. No. 4.5e-66;
0; Mismatches 66;
                                                                                                               Nucleotide sequence of a human polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 113-114; 140pp; Japanese
                                                                                                                                                                                                                                   location/Qualifiers
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 BP.
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ilarity 81.3%;
Conservative
AAH74285 standard; DNA; 411
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                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 course of the invention.
                                                                                                                                                                                                                                                                                                                               /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suzuki M,
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Best Local Similarity
Matches 339; Conserv
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                                                                                                                                                                                         Homo sapiens
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                                     AAH74285;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-JAN-2001
                                                                                 339;
                                                              Query Match
Best Local S:
Matches 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a stabilised composition of an antibody which recognises parathyroid hormone-related peptide (PTHLP) - see AAG64793. The composition consists of a solution of the antibody in a buffer of pH 5-8 containing one or more of acetic acid, phosphoric acid, citric acid and their salts. The composition has increased storage stability, especially at elevated temperatures. The composition antagonises the action of PTHLP, and may be used in the treatment of diseases involving disturbances of calcium regulation (high or low serum calcium concentration) such as humoral hypercalcaemia of malignancy and as an analgesic. The present sequence represents DNA encoding a humanised
                                                                                                                                                                                                                           Parathyroid hormone-related peptide; PTHrP; antagonist; antibody; calcium regulation disorder; serum calcium concentration; heavy chain; humoral hypercalcaemia of malignancy; cytostatic; analgesic; humanised;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for treating diseases of calcium regulation and for use as an analgesic, comprises an antibody recognizing parathyroid hormone
tatccagacagtgtgaaggggcgattcaccatctccagagacaattccaagaacacgctg 294
                                                                        ACTACAGGGTCTGAC-----TCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                     TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGGCTTG
                               /product= "Heavy chain precursor"
/note= "No stop codon given in the specification"
1..57
                                                                                                                                                                                                      Humanised anti-PTHrP Ab heavy chain version a DNA, SEQ ID NO:58.
                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
/product= "Mature heavy chain"
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58..411
/*tag=
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Chimeric - Homo sapiens.
Synthetic.
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                                                                                                                                                                                 08-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
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version of the heavy chain of anti-human PTHrP murine monoclonal antibody 23-57-137-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTCCAGGGCAGGGGCTGGAGTGGGTCTCCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGGAACGCCAACAACACACTG 300
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                                                                                                                                                                                                                  12;
                                                                                                                                                                 Length 411;
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                                                                                         A; 98 C; 128 G; 103 T; 0 other
                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                  99
                                                                                                                                                                 Score 267.4; DB 2
Pred. No. 4.5e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human antibody H chain protein SEQ ID NO:58.
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                                                                                                                                                                 65.1%;
llarity 81.3%;
Conservative
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                                                  The present invention describes an agent (I) for ameliorating low vasopressin levels, and symptoms caused by this depression, containing as an active component a substance which inhibits the binding of parathyroid hormone related peptide (PTHrP) to its receptor. (I) has antidiarrheic, antiemetic, antidiabetic and antipyretic activities. (I) can be used for the amelioration of symptoms caused by decrease in vasopressin levels, such as that due to cancer are treated using the agent. These symptoms include dehydration, excessive urination, thirst, vomiting, diarrhoea, fever, perspiration and diabetes. AAF69085 to AAF69140 and AAB76879 to AAB76877 represent sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTTGAAAGGTGTCCAGTGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 411;
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                                                                                                                                                                                                                                                                                                                            Score 267.4; DB 42.
                                                                                                                                                                                                                                                                                              Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human antibody H chain protein SEQ ID NO:58.
                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                  Page 90-91; 114pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                       65.1%;
81.3%;
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Best Local Similarity 81.3<sup>s</sup>
Matches 339, Conservative
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                    Example
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The present line into incention again, again (1) to the Leadumin and prevention of diseases other than hyperclacemia associated with parathyroid hormone (PTH) or parathyroid hormone related peptide (PTHPP).

(I) contains as an active component a substance which promotes or inhibits the binding of ligands to PTH receptor or PTHPP receptor or is an agonist or antagonist to these receptors. (I) have analgesic, or is an agonist or antagonist to these receptors. (I) have analgesic, immunosuppressive, mootropic, neuroprotective, antiinfammatory, cycostatic, antithyroid, eating-disorders and cardiovascular activities.

(I) is used for treatment and prevention of disorders associated with PTH or PTHPP, including: pain; immune suppression, disturbances of the diseast, blood chemistry, thyroid function, and electrolyte balance; central nervous system disorders such as sleep disturbance, meurological disturbance, brain function disturbance; brain function disturbance; and disorders caused by PTH or PTHPP associated cytokine cascade including blood poisoning, dropsy, inflammation, blood disease, calcium disturbance and autoimmune disease.

Creatment and prevention of disorders other than hypercalcaemia which are associated with PTH or PTHPP especially those associated with malignant tumours, and thereby ameliorating the quality of life of these patients. AAR69141 to AAR69198 to AAR8691 to Expresent
                                                                                                                                                                                                                                                                                                      or parathyroid hormone related peptide receptor for treatment of disorders associated with parathyroid hormone other than hypercalcemia
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                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes an agent (I) for the treatment and
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                                                                                                                                                                                                                                                                                   parathyroid hormone
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                                                                                                                                                                                                        Azuma
                                                                                                                                                                                                      Saito H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
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Pred. No. 4.5e-66;
                                                                                                                                                                                                                                                                                 Agents modifying the binding of ligands to
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                                                                                                                                                                                                      Tsunenari T,
                                                                                                                                                                                                                                                                                                                                                                                   Example; Page 101-102; 130pp; Japanese.
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Best Local Similarity 81.3%;
Matches 339; Conservative
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                                                                                                                      99JP-0189793
                                                                             03-JUL-2000; 2000WO-JP04414
                                                                                                                                                              (CHUS ) CHUGAI SEIYAKU KK
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WO200102011-A1
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Agents inhibiting binding of parathyroid hormone related peptide to its receptor for treatment of drug-resistant hyperglycemia \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, mouse, drug-resistant hyperglycaemia; PTHrP, cardiovascular; parathyroid hormone related peptide; gastrointestinal; cancer; central nervous system; calcium-antagonist; bone resorption inhibitor; bisphosphonate; calcitonin; calcium elimination promoter; intestinal calcium absorption inhibitor; ds.
tatetgcaaatgaacagcetgagagetgaggacacggetgtgtattactgtgcgagacag 354
                                                                        361 ACTACAGGGTCTGAC----TCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                                                                                                                 Sequence 411 BP; 82 A; 98 C; 128 G; 103 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human antibody H chain protein SEQ ID NO:58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 95-96; 118pp; Japanese.
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immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;
anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;
antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;
thrombolytic; immunogen; antibody; gene therapy; neurological disorder;
Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein levels, as tissue markers, and to isolate receptors or ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; Antianaemic; osteopathic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                             ACTACAGGGTCTGAC-----TCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                                                                                                                                                                                                                                             TITCTICAAAIGAACAGCCIGAGAGCIGAGGACACGCCIGICIAIIACTGIGCGAGCIIG
     GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG
                                                                          241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGCCAACAACACCTG
                                                                                                                                                                                          tatctgcaaatgaacagcctgagagctgaggacacggctgtgtattactgtgcgagacag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cDNA encoding a novel human protein #191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 432-434; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                             AAS22625 standard; cDNA; 1458 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel protein;
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DB 22; Length 411; Indels

4.5e-66; -rhes 66;

Score 267.4; I Pred. No. 4.5e-0; Mismatches

Query Match 65.1%; Best Local Similarity 81.3%; Matches 339; Conservative

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TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180

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Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-versus-host disease, eczema, heamophilla, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence encodes a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GIGCAGCIGGTGGAGTCTGGGGGGGCGTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                         GCTCCAGGGCAGGGGCTGGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
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                                                                                                                                                                                                                                                                   Length 1458;
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                                                                                                                                                                                                               Sequence 1458 BP; 353 A; 369 C; 368 G; 364 T; 4 other;
                                                                                                                                                                                                                                                                Score 266; DB 22;
Pred. No. 1.7e-65;
0; Mismatches 55;
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Best Local Similarity 83.8%;
Matches 315; Conservative
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	4	7	3, A	100,	100,	97, 4	97,	264,	264,	9891,		5766	58,	58,	58,	58,	58,	193,	193,	939	945		•	Sequence 5795, Ap	_	m	Sequence 1849, Ap	13	72,	73	Sequence 73, Appl
Ω		-292-0	-343-4	US-09-617-746A-100	-631-7		US-09-631-451A-97	US-09-359-922-264	US-09-359-922-264	US-09-652-127-9891	US-09-698-010-15656	9	US-09-269-332-58	US-09-423-800-58	-501-5	US-10-019-571-58	US-10-019-785-58	US-09-617-746A-193	US-09-631-451A-193	US-09-652-125A-9393	US-09-652-127-9452	_	US-09-699-999-7481	US-09-710-281-5795	US-09-716-475-7305	US-09-726-175-3019	US-09-726-176-1849	US-09-726-211-1347	0	US-09-668-317-73	US-10-105-891-73
BB	14	16	17	23	24	23	24	17	17	25	27	28	16	18	37	37	37	23	24	25	25	25	27	28	28	29	59	•29	-		38
% Query Match Length	411	411	19040	1710	1710	1721	1721	1709	1709	591	591	591	411	411	411	411	411	1458	1458	3041	3041	3041	3041	3041	3041	3041	3041	3041	645	069	069
% Query Match	100.0	99.5	87.2	68.8	68.8	68.8				66.7	66.7	66.7	65.1	65.1	65.1	65.1	65.1	64.7	64.7	64.7	64.7	64.7	4	64.7	64.7	マ	64.7	64.7	64.5	64.5	64.5
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APPLICANT: REFF, MITCHELL E.
APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: KLOETZER, WILLIAM S.
APPLICANT: NAKAMINGA, TAKEHIKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
FILE REPERENCE: 2352.0699
CURRENT APPLICATION NUMBER: U5/09/292,053
CURRENT APPLICATION NUMBER: 08/803,085
PRIOR APPLICATION NUMBER: 08/803,085
PRIOR APPLICATION NUMBER: 08/803,085
PRIOR PILING DATE: 1997-02-20
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                 61 GTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120
                                                                                                                                                                          TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
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                                                     1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTTGAAAGGTGTCCAGTGTGAGG 60
                                                                      61 GTGCAGCTGGTGGAGTCTGGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
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Pred. No. 2e-103;
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          ilarity 100.0%; P
Conservative 0;
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LOCATION: (1) .. (58)
NAME/KEY: met_peptide
LOCATION: (58) .. (411)
NAME/KEY: CDS
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          Best Local Similarity
Matches 411; Conserv
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Matches 409; Conserv
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US-09-292-053-7
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    Sequence 21418, A Sequence 2415, Ap Sequence 2415, Ap Sequence 10, Appl Sequence 1172, Ap Sequence 98, Appl Sequence 9, Appli Sequence 9, Appli Sequence 3094, Ap Sequence 3094, Ap Sequence 14, Appl Sequence 14, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: ALEGALIALES
STATE: VIRGINIA
ZOUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/019,441
FILING DATE: 05-Feb-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. Box 1404
CITY: Alexandria
               US-09-491-404-2415
US-09-922-279-2415
US-09-922-279-2415
US-09-922-279-2415
US-09-203-978-415
US-09-203-972-4372
US-09-617-746A-98
US-09-617-746A-98
      US-09-431-517-21418
                                                                                                                                                                    US-09-922-279-3094
US-09-922-279A-3094
US-09-844-684-14
                                                                                                                                       US-08-471-986-9
US-09-491-404-3094
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APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:

NAME: TESKIN, RObin L.

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                              ALIGNMENTS
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SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09019441
GENERAL INFORMATION:
APPLICANT: REFF, Mitchell E.
KLOFTZER, William S.
NAKAMURA, Takehiko
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TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 58..411
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INFORMATION FOR SEQ ID NO: 4:
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Gaps

us-09-019-441-4.rnpm

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361 ACTACAGGGTCTGACTCCTGGGCCCAGGGAGTCCTGGTCACCGTCTC 407
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Chen, Rui-hong
Asundi, Vinod
Cao, Yicheng
Tillinghast, John
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Best Local Similarity 82.8%;
Matches 337; Conservative (
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Qian, Xiaohong
                                                                                                                                                                                                                          APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenqhua
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; LOCATION: (162)..(1253)
US-09-617-746A-100
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US-09-617-746A-100
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APPLICANT: BARNETT, RICHARD S.
APPLICANT: BARNETT, RICHARD S.
APPLICANT: BARNETT, RICHARD S.
APPLICANT: MCLACHLAN, KAREN R.
ITILE OF INVENTION: NOVEL METHOD FOR INTEGRATING GENES AT SPECIFIC SITES IN TITLE OF INVENTION: WAMMALIAN CELLS VIA HOMOLOGOUS RECOMBINATION AND TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
TITLE OF INVENTION: VECTORS FOR ACCOMPLISHING THE SAME
CURRENT APPLICATION NUMBER: 08/09/343,485A
CURRENT FILING DATE: 1999-06-30
PRIOR FILING DATE: 1999-02-13
PRIOR PELLORING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PARENTIN VET. 2.1
SEQ ID NO 3
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                                                                                                                                                                                     121 tgcgcagcctccgggttcaggttcaccttcaataactactacatggactgggtccgccag
                                                                               TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGAACGCCAACAACACACTG
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TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG
                                                             GCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCCACATGG
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Pred. No. 2.2e-88;
0; Mismatches 26
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93.4%;
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Best Local Similarity 93.4 Matches 385; Conservative
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LENGTH: 19040
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                                                                 282 tgtgcagcctctg-----gattcacctttagcagtttttcgatgagctgggtccgccag
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                                           TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG
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                                                                                                                                                              361 ACTACAGGGTCTGACT-CCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 282.6; DB 2
Pred. No. 1.3e-67;
0; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: POlypeptides FILE REPERENCE: 1272-017CIP2A (785CIP2A); CURRENT APPLICATION NUMBER: 05/09/617,746A CURRENT FILING DATE: 2000-01-25 NUMBER: OF SEQ ID NOS: 220 SEQ ID NO 100
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61 GTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGAACGCCAACAACACACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 tacgcagactccgtgaagggccggttcaccatctccagagacaattccaagaacacgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1721;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.8%; Score 282.6; DB 382.8%; Pred. No. 1.3e-67; ive 0; Mismatches 64
                                                                                                                                                                                    APPLICANT: Wang, Zhiwel APPLICANT: Chen, Rul-hong APPLICANT: Cao, Mul-hong APPLICANT: Cao, Yicheng APPLICANT: Tillinghast, John APPLICANT: Tillinghast, John APPLICANT: Drmanac, Radoje T. TITLE OF INVENTION: Novel Nucleic Acids and TITLE OF INVENTION: POlypeptides FILE REFERENCE: 21272-017CIP2A (785CIP2A) CURRENT APPLICATION NUMBER: US/09/617,746A CHENENT APPLICATION NUMBER: 09/491,404 PRIOR APPLICATION NUMBER: 09/491,404
   Application US/09617746A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 97, Application US/09631451A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: pt_FL_genes Version 1.0 SEQ ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 82.8
Matches 337; Conservative
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APPLICANT: Liu, Chenghua
APPLICANT: Zhou, Ping
APPLICANT: Qian, Xiaohong la
                                                                                                                                                                Qian, Xiaohong
                                                                   APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: (162)..(1085)
US-09-617-746A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                             Zhou, Ping
                                      GENERAL INFORMATION
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US-09-631-451A-97
   Sequence 97,
                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
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64; Indels
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Pred. No. 1.3e-67;
0; Mismatches 64
                                                                                                                                                                                                                                                                                              APPLICANT: Alou, Chelyllud
APPLICANT: Abou, Ping
APPLICANT: Abou, Ping
APPLICANT: Glan, Xiaohong B.
APPLICANT: Ghen, Rui-hong
APPLICANT: Asundi, Vinod
APPLICANT: Asundi, Vinod
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 785CIP2B
CURRENT APPLICATION NUMBER: US/09/631,451A
CURRENT APPLICATION NUMBER: 09/617,746
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-07-17
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 220
SEQ ID NO 100
SEQ ID NO 100
SEQ ID NO 100
SEQ ID NO 100
                                                                                                                                                                                    Sequence 100, Application US/09631451A GENERAL INFORMATION:
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82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.8%
Best Local Similarity 82.8%
Matches 337; Conservative
                                                                                                                                                                                                                                              APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (162)..(1253)
US-09-631-451A-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                       RESULT 5
US-09-631-451A-100
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US-09-617-746A-97
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APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: LIBRARIES

TITLE OF INVENTION: LIBRARIES

FILE REFERENCE: 20411-752CON1

CURRENT APPLICATION NUMBER: US/09/359,922

CURRENT FILING DATE: 1999-07-22

EARLIER FILING DATE: 1999-12-03

NUMBER OF. SEQ ID NOS: 13203

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 264
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                              APPLICANT: Cao, Yicheng
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: NOVEL Nucleic Acids and
TITLE OF INVENTION: NOVEL Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 785CIP2B
CURRENT APPLICATION NUMBER: 05/09/631,451A
CURRENT FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-25
NUMBER OF SEQ ID NOS: 220
SOFTWARE: PL-FL-genes Version 1.0
SEQ ID NO 97
LENTH: 1721
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; Sequence 264, Application US/09359922
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 82.8
Matches 337; Conservative
Chen, Rui-hong
Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (162)..(1085)
US-09-631-451A-97
                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT:
                     APPLICANT
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: LESHKOWITZ, Dena
APPLICANT: LESHKOWITZ, Dena
TITLE OF INVENTION: LIBERRIES
TITLE OF INVENTION: LIBERRIES
FILE REPERENCE: 20411-752COM1
CURRENT APPLICATION NUMBER: US/09/359,922A
CURRENT FILING DATE: 1999-07-22
EARLIER PILING DATE: 1998-12-03
EARLIER PILING DATE: 1998-12-03
EARLIER PILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 13203
SOFTWARE: FASTSEQ for Windows Version 3:0
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Pred. No. 5.3e-66;
0; Mismatches 52; Indels
                                                                                    Score 276.8; DB 17; Length
Pred. No. 5.3e-66;
0; Mismatches 52; Indels
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Best Local Similarity 82.1%;
Matches 353; Conservative
                                                                                    67.3%;
illarity 82.1%;
Conservative
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-359-922-264
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US-09-359-922-264
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Best Local Similarity
Matches 353; Conserv
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LENGTH: 1709
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Sequence 981, Application US/09652127

GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREOR
FILE REFERENCE: 1600.1183-001
CURRENT APPLICATION NUMBER: US/09/652,127
FRIGH SPPLICATION NUMBER: 06/191,134
PRIOR FILING DATE: 2000-08-30
NUMBER OF SEQ ID NOS: 10475
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Si
Matches 345;
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361 ACTACAGG-----TCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA
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GENERAL INFORMATION:
APPLICANT: Williamson, Mark
APPLICANT: Shylan, Andrew W.
TITLE OF INVENTION: THEREFOR FILE OF INVENTION: THEREFOR FILE OF INVENTION: THEREFOR FILE OF INVENTION: 1400.2029-001
CURRENT APPLICATION NUMBER: US/09/698,010
CURRENT FILING DATE: 2000-10-27
PRIOR PILING DATE: 1999-10-29
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Pred. No. 2.4e-65;
0; Mismatches 60;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15656
LENGTH: 591
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GENERAL INFORMATION:
APPLICANT: Hunter, John J.
APPLICANT: Shyjan, Andrew W.
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82.1%;
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Best Local Similarity 82.1
Matches 345; Conservative
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SEQ ID NO 58
FEATURE:
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APPLICANT: WAKARARA, YUJI
APPLICANT: WAKARARA, YUJI
APPLICANT: YABUTA, NAOHIBO
TITLE OF INVENTION: ANTIBODY AGAINST HUMAN PARATHORMONE RELATED PEPTIDES
FILE REFERENCE: 04853-0033
CURRENT PAPLICATION NUMBER: US/09/269,332
CURRENT FILING DATE: 1997-09-24
PRIOR PILING DATE: 1997-09-24
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1996-09-26
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
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Pred. No. 2.4e-65;
0; Mismatches 60; Indels 1
                 TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES TITLE OF INVENTION: THEREPOR TELLE REFERENCE: 1600.2036-001
CURRENT APPLICATION NUMBER: US/09/710,281
PRIOR APPLICATION NUMBER: 60/11-10
PRIOR APPLICATION NUMBER: 60/164,254
PRIOR FILING DATE: 1999-11-09
                                                                                                                            NUMBER OF SEQ ID NOS: 5803
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5766
LENGTH: 591
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Best Local Similarity 82.1%;
Matches 345; Conservative
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SOFTWARE: Patentin Ver. 2
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US-09-710-281-5766
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LENGTH: 411
    APPLICANT:
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GCTCCAGGGCAGGGCCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
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                                                                                                                                                                                      1.5e-63;
ches 66; Indels
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Pred. No. 1.5e-
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: SATO, WO:
APPLICANT: SATO, WILL
APPLICANT: TSUNINARI, TOSHIAKI
APPLICANT: ISHII, KIMIE
TITLE OF INVENTION: CACHEXIA REMEDY
FILE REFERENCE: 04853-0036
CURRENT APPLICATION NUMBER: US/09/423,800
CURRENT FILING DATE: 1999-11-12
PRIOR PRILING DATE: 1998-05-13
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1997-05-15
PRIOR FILING DATE: 1997-05-15
PRIOR PRILING DATE: 1997-05-15
PRIOR FILING DATE: 1997-05-15
PRIOR FILING DATE: 1997-07-18
                                                                                                                                                                         Query Match 65.1%;
Best Local Similarity 81.3%;
Matches 339; Conservative
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LOCATION: (1)...(411)
NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; NAME/KEY: mat_peptide
; LOCATION: (58)...(411)
US-09-269-332-58
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NAME/KEY: CDS
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LOCATION:
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GENERAL INFORMATION:
APPLICANT: CHUGAI SETYAKU KABUSHIKI KAISHA
TITLE OF INVENTION: Ameliorative agent for low vasopressin concentration
FILE REFERENCE: PH 944-PCT
CURRENT APPLICATION NUMBER: US/10/019,501
CURRENT FILING DATE: 2001-12-31
PRIOR FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                   GTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
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                                      Length 411;
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                                   Score 267.4; DB 18; Length
Pred. No. 1.5e-63;
0; Mismatches 66; Indels
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                                   65.1%;
81.3%;
                                 Query Match
Best Local Similarity 81.3*
Matches 339; Conservative
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Best Local Similarity 81.3
Matches 339; Conservative
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; LOCATION: (1)..(411)
; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
US-10-019-501-58
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ORGANISM: Homo sapiens
US-09-423-800-58
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US-10-019-501-58
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82, Appl 16290, A

187, App 21308, A 20914, A 25, Appl

Sequence 1, Appli Sequence 16675, A

Sequence Sequence

Run on:

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RESULT 1

Sequence 4, Application US/10103686

Sequence 4, Application US/10103686

GENERAL INFORMATION:

KLOETZER, Milliam S.

NARAMURA, Takehiko

TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL

AMTIBODIES AND USE THEREOF AS THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTY: United States
IP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/103,686
FILING DATE: 25-MAT-2002
CHASSIFICATION: CURROWN>
US-10-206-008-401
US-10-211-364-212
PCT-US02-18947-1932
US-10-172-118-1932
PCT-US02-20332-75
US-10-206-008-198
PCT-US02-20332-79
US-10-216-008-411
US-10-213-86-318
PCT-US02-20332-82
US-10-212-95-16290
US-10-205-008-187
US-10-205-008-187
US-10-203-136-21308
US-10-203-136-21308
PCT-US02-11853-16
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US-09-918-995-16675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703) 836-2021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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LENGTH: 411 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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(without alignments)
1998.488 Million cell updates/sec
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Sequence 4, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 12, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 16557, A
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Sequence 1, A
Sequence 1, A
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Sequence 1, A
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Sequence 14,
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/cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
/cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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US-09-634-754C-28
US-09-634-754D-28
US-09-918-995-16657
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US-10-146-502-2106
US-10-158-646-54
US-09-511-939-1
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US-10-220-149-58
US-10-125-237-73
PCT-US02-2018-11
US-10-040-244-10
US-10-040-244-12
US-10-040-244-12
US-10-26-008
US-10-153-382-1
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US-09-968-561A-1
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US-10-153-382-2
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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length: 2000000000
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Maximum DB seq
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APPLICANT: CHIMIAN SELVAKU KABUSHIKI KAISHA
TITLE OF INVENTION: THERAPEUTIC AND PREVENTIVE AGENTS FOR DENTAL DISEASES
TILE REPERBENCE: PH-1092-PCT
CURRENT APPLICATION NUMBER: US/10/182,018
CURRENT FILING DATE: 2002-07-24
PRIOR PRICATION NUMBER: UP 2000-83034
PRIOR FILING DATE: 2000-83034
                                                          1426 TGTGCAGCCTCTG----GATTCACCTTCAATGATTATGCCATGAGCTGGGTCCGCCAG 1373
                                                                                                                  1252 TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATACTGTGCGAGAGA 1193
                                                                                                                                                                                                  1312 TACGCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAACTCACTG 1253
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                                                                                              GCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
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Pred. No. 1.7e-58;
0; Mismatches 66;
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Best Local Similarity 81.3%;
Matches 339; Conservative
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) LOCATION: (58)..(411)
US-10-182-018-58
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US-10-182-018-58
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LENGTH: 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL CONTIGS OBTAINED FROM VARIOUS CDNA TITLE OF INVENTION: LIBRARIES FILLE REFERENCE: 20411-752COIN CURRENT APPLICATION NUMBER: US/09/919,002 CURRENT FILING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: US/99-07-22 PRIOR FILING DATE: FILING DATE: 1999-07-22 PRIOR FILING DATE: FILING DATE: 1999-07-22 PRIOR FILING DATE: FILING DATE: 1999-07-22 PRIOR FILING DATE: FILING DATE: 1999-07-22
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Pred. No. 7.6e-61;
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                                                                                       100.0%; Score 411; DB 7;
llarity 100.0%; Pred. No. 4.7e-95;
Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 3.0
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LOCATION: 58..411
SEQUENCE DESCRIPTION: SEQ ID
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82.1%;
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Best Local Similarity 82.1
Matches 353; Conservative
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US-09-919-002-264
                                                                                                         Similarity
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US-09-919-002-264/c
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US-10-103-686-4
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LENGTH: 1709
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Best Local S
Matches 411
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
                CHUGAI SEIYAKU KABUSHIKI KAISHA
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81.3%;
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Best Local Similarity 81.3
Matches 339; Conservative
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Xue, Aidong J.
Zhang, Jie
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Wang, Jian-Rui
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Asundi, Vinod
Ren, Feiyan
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APPLICANT: Liu, Chenghua
                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                           ; NAME/KEY: mat_peptide
; LOCATION: (58)..(411)
US-10-169-003-58
                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (1)..(411)
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                                            TITCTICAAAIGAACAGCCIGAGAGCIGAGACACGGCIGICIAIIACIGIGCGAGCIIG 360
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                                                          235 tatccagacagtgtgaaggggcgattcaccatctccagagacaattccaagaacacgctg
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INFORMINE TISSUE degradation inhibiting agent FILE REFERENCE: PH-1015-PCT
CURRENT APPLICATION NUMBER: US/10/220,149
CURRENT FILING DATE: 2002-08-27
PRIOR APPLICATION NUMBER: JP2000-52414
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 267.4; DB 6;
Pred. No. 1.7e-58;
0; Mismatches 66;
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81.3%;
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Best Local Similarity 81.33
Matches 339; Conservative
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TITLE OF INVENTION: Stabilized Antibody Composition and Pharmaceutical Preparation TITLE OF INVENTION: Injection TITLE OF INVENTION: Injection FILE REFERENCE: PH-1093-PCT CURRENT APPLICATION NUMBER: 2002-06-26 PRIOR FILING DATE: 2002-06-26 PRIOR FILING DATE: 1999-12-28 NUMBER OF SEQ ID NOS: 75 NUMBER: Patentin Ver. 2.0 SEQ ID NO 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 267.4; DB 7;
Pred. No. 1.7e-58;
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APPLICANT: FORCE, WALKER F.
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI
TITLE OF INVENTION: 1SOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI
FILE REFERENCE: 021286/0272501
CURRENT APPLICATION NUMBER: 05/10/040,244
PRIOR FILING DATE: 2000-44-28
PRIOR PLILING DATE: 2000-44-28
PRIOR RILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 9CT/US01/13672
PRIOR PLILING DATE: 2001-04-27
PRIOR APPLICATION NUMBER: 09/844,684
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                                24; Gaps
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                                                                                                            14 atggagtttgggctgagctggctttttcttgtggctattttaaaaggtgtccagtgtgag 73
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85.7%; Pred. No. 4e-57;
iive 0; Mismatches 45; Indels
                                Indels
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                              0; Mismatches
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GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn Ver. 3.0
        Best Local Similarity 80.2 Matches 344; Conservative
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Matches 305; Conservative
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US-10-040-244-10
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Score 265.2; DB 7
Pred. No. 6.3e-58;
0; Mismatches 43
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APPLICANT: Boyle, William J
APPLICANT: Martin, Francis H
APPLICANT: Corvalan, Jose
APPLICANT: Corvalan, Jose
APPLICANT: Corvalan, Jose
TITLE OF INVENTION: Antibodies to OPGL
FILE REFERENCE: 06843.0049-00000
CURRENT APPLICATION NUMBER: PCT/USO2/20181
CURRENT FILING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: 60/301,172
PRIOR APPLICATION NUMBER: 60/301,172
PRIOR PILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 791CIPADIN:
CURRENT APPLICATION NUMBER: US/10/125,237
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 09/668,317
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-04-18
NUMBER: OF SEQ ID NOS: 91
SEQ ID NO 73
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86.2%;
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US-10-125-237-73
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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PCT-US02-20181-1
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APPLICANT: FORCE, WALKER F.
APPLICANT: TARAHASHI, NOBUAKI
APPLICANT: MIKAYAMA, TOSHIFUMI
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI
TITLE OF INVENTION: 1SOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTI
FILE REFERENCE: 021286/0272501
CURRENT APPLICATION NUMBER: 05/200,601
PRIOR APPLICATION NUMBER: 60/200,601
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 17
SSOFTWARE: PATENTIN VET: 3.0
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PPZ53CIN
CURRENT APPLICATION NUMBER: US/10/206,008
CURRENT FILING DATE: 2002-07-29
PRIOR APPLICATION NUMBER: 09/760,479
PRIOR FILING DATE: 2001-01-16
PRIOR PLILOATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/19,065
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
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Pred. No. 4.7e-56;
0; Mismatches 47
                                                            US-10-040-244-12; Sequence 12, Application US/10040244; GENERAL INFORMATION: APPLICANT: KIRIN BEER KABUSHIKI KAISHA APPLICANT: FORCE, WALKER F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 189, Application US/10206008 GENERAL INFORMATION:
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85.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: TAKAHASHI, NOBUAKI
APPLICANT: MINAYAMA, TOSHIPUMI
TITLE OF INVENTION: TSOLATION AND CHARACTERIZATION OF HIGHLY ACTIVE ANTI-CD40 ANTIBOD
FILE REFERENCE: 021286/0272501
CORRENT APPLICATION NUMBER: 05/10/040,244
CURRENT FILING DATE: 2002-06-17
PRIOR FILING DATE: 2000-4-28
PRIOR APPLICATION NUMBER: 60/200, 601
PRIOR APPLICATION NUMBER: 09/844,684
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN VEY: 3.0
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                                                              206 gctccagggaaggggctggtgtgggtctcacgtattaatagtgatgggagtagcacaacc
                                      TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG
                                                                                                                     GCTCCAGGGCAGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCCACATGG
                                                                                                                                                                                                   241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGGAACGCCAACAACACACTG
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                                                                                                                                                                                                                                                                                                              63.5%; Score 261; DB 7; Length 630;
85.6%; Pred. No. 7.3e-57;
.ive 0; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/10040244
GENERAL INFORMATION:
APPLICANT: KIRIN BEER KABUSHIKI KAISHA
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Best Local Similarity 85.6
Matches 304; Conservative
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US-10-040-244-14
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LENGTH: 630
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ER: 60/214,88 ER: 60/217,48 D-07-11 D-07-11 ER: 60/225,75 D-08-14 ER: 60/220,96 ER: 60/217,49 ER: 60/217,49 ER: 60/217,49 ER: 60/217,49 ER: 60/217,49 ER: 60/218,29 D-08-14 ER: 60/225,75	11. 60/224, 51. 60/224, 51. 60/224, 51. 60/225, 26. 60/216, 88. 60/216, 88. 60/216, 88. 60/225, 27. 60/251, 86. 60/234, 27. 60/228, 92. 60/228, 92. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/224, 51. 60/220, 96. 61. 61. 61. 61. 61. 61. 61. 61. 61. 6	
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PRIOR FILING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/231,413
PRIOR PILLING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/235,509
PRIOR PILLING DATE: 2000-09-05
PRIOR APPLICATION NUMBER: 60/237,039
PRIOR PAPLICATION NUMBER: 60/237,037
PRIOR PAPLICATION NUMBER: 60/237,040
PRIOR PAPLICATION NUMBER: 60/239,335
PRIOR PAPLICATION NUMBER: 60/239,335
PRIOR PAPLICATION NUMBER: 60/239,337
PRIOR PAPLICATION NUMBER: 60/239,210
PRIOR PAPLICATION NUMBER: 60/239,211
PRIOR PAPLICATION NUMBER: 60/2

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GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                 APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
CURRENT APPLICATION NUMBER: US/10/153,382
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
PRIOR FILING DATE: 2001-05-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10153382 GENERAL INFORMATION:
                                                                                                                                                              US-10-153-382-1; Sequence 1, Application US/10153382; GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 79.4
Matches 331; Conservative
                      397 GTCACCGTCTCCTC 410
                                               480 gtcaccgtctctc 493
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US-10-153-382-4
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            PRIOR FILING DATE: 2000-11-17
PRIOR PELICATION NUMBER: 60/249,214
PRIOR APPLICATION NUMBER: 60/249,214
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-11-17
PRIOR PELING DATE: 2000-09-14
PRIOR PILING DATE: 2000-09-14
PRIOR PELING DATE: 2000-09-08
PRIOR APPLICATION NUMBER: 60/232,081
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 60/233,064
PRIOR PILING DATE: 2000-09-14
PRIOR PILING DATE: 2000-10-20
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APPLICATION NUMBER: 60/231,243
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PRIOR APPLICATION NUMBER: 60/233,065
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/10153382
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR APPLICATION NUMBER: 60/293042
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 253.2; DB 7;
Pred. No. 7.6e-55;
0; Mismatches 73;
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Best Local Similarity 79.0%;
Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1395
                                                                                                                                                                                                                                                                                           RESULT 15
US-10-153-382-8
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                                                                                       Length 1392;
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                                                                                         DB 7;
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GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVERTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 254.6; DB 7
Pred. No. 3.4e-55;
0; Mismatches 74
                                                                                                       Pred. No. 3.3e-55,
                                                                                                                       0; Mismatches
                                                                                         Score 254.6;
                                                                                       61.9%;
79.4%;
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79.48;
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SOFTWARE: Patentin Ver. 2.1
                                                                                                       Best_Local Similarity 79.4
Matches 331; Conservative
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Best Local Similarity 79.4
Matches 331; Conservative
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US-10-153-382-2
                         ); ORGANISM: Homo sapiens
US-10-153-382-4
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LENGTH: 1392
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US-10-153-382-2
              TYPE: DNA
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Search completed: September 23, 2002, 19:58:58 Job time: 7188 sec

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APPLICANT: KLOETZER, William S.
APPLICANT: NARAWURA, Takehiko
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
TITLE OF INVENTION: ANTIBODIES AND USE THEREOF AS THERAPEUTICS
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                         Sequence
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
US-08-653-402B-5
US-08-545-809A-53
US-08-545-809A-21
US-08-545-809A-20
US-08-053-171-10
US-08-053-171-6
US-08-619-491-3
PCT-US95-07302-3
US-08-545-809A-9
US-08-545-809A-30
US-08-157-101A-6
US-08-157-101A-1055-35
US-08-1055-35
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                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-353
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/803,085
FILING DATE: 20-FEB-1997
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-803-085-4; Sequence 4, Application US/08803085; Patent No. 601138; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
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nucleic acid
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FEATURE:
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; LOCATION:
US-08-803-085-4
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   RESULT
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                                                                                                                                                                                                                                             1 ATGGAGTTTGGGCTGAGCTG......TCCTGGTCACCGTCTCCTCA 411
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                                        Compugen Ltd
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US-08-468-671-3
US-08-468-671-1
US-08-545-809A-21
US-08-545-809A-48
US-08-134-346A-49
US-08-134-346A-49
US-08-134-346A-29
US-08-545-809A-13
US-08-545-809A-23
US-08-545-809A-23
US-08-545-809A-23
US-08-545-809A-23
US-08-545-805A-23
US-08-545-805A-23
US-08-54-515-7
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US-08-545-809A 64
US-08-452-164A-56
US-08-452-164A-56
US-08-10-930B-27
US-08-976-28A-27
US-08-862-124-1
US-08-862-124-3
US-09-862-124-3
US-09-873-8839A-9
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5-08-652-816A-21
5-08-652-816A-22
5-08-652-816A-22
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                     GenCore version 4.5 Copyright (c) 1993 - 2000 Com
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                                                                                                                                September 23, 2002, 18:00:53
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Listing first 45 summaries
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/function= "Heavy Chain"
/product= "Immunoglobulin Variable Region"
/standard_name= "HuMab L612 Heavy Chain Variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCCAGGGCCAGGGGCTGGAGTCGCTATTAGTAGTAGTGGTGATCCCACATGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGCGCCAACAACACACTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          355 GGCAACGATATTTGACTTGTTATGCTTGGGGCCAGGGAACCCTGGTCACCGTCTCC 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGAGTTTGGCTGACCTGGCTTTTTCTTGTGGCTAATTTAAAAGCTGTCCAGTGTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235 TACGCAGACTCCGTGAAGGCCGGTTCACCATCTCCAGAGACAATCCAAGAACACGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TGTGCAGCCTCTG----GATTCACCTTTAGCAGCTGTGCCATGAGCTGGGTCCGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTCTTCAAATGAACAGCCTGAGAGCTGAGACACGGCTGTCTATTACTGTGCGA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 TATCTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----GCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACGGTCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature

LOCATION: 397..429

OTHER INFORMATION: /function= "Complementary determining oTHER INFORMATION: region 3 (CDR3)"

US-08-026-320A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 271..300
OTHER INFORMATION: /function= "Complementary
OTHER INFORMATION: determining region 2 (CDR2)"
                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 148..162
OTHER INFORMATION: /function= "Complementary
OTHER INFORMATION: determining region 1 (CDR1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 63.2%; Score 259.8; DB 1; Best Local Similarity 79.9%; Pred. No. 1.5e-67; Matches 338; Conservative 0; Mismatches 67;
                                                                                                               ORGANISM: Homo sapiens
CELL TYPE: Epstein Barr Virus Transformed B
CELL LINE: L612
                                                                                                                                                                                                                                                                                                            Region Sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08259372A
                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /sta
OTHER INFORMATION: Regi
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature LOCATION: 271..300
                                                                                                                                                                                                                          LOCATION: 1..432
OTHER INFORMATION:
      TOPOLOGI.
MOLECULE TYPE: CDN
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                     OTHER INFORMATION
           linear
                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |||
TCA 417
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                                                                                                                                                                                 FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                   121 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACATGGACTGGGTCCGCCAG 180
                                                                                                                                                                                                                                                                                                                                                     181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCCACATGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAACGCCAACAACACACTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGTGCGAGCTTG 360
                                                  Gaps
                                                                                                                 1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
         Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08026320A

Batent No. 5419904

GENERAL INFORMATION:
APPLICANT: ITIE, Reiko F

TITLE OF INVENTION: UNMAN B-LYMPHOBLASTOID CELL LINE
TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 11
100.0%; Score 411; DB 3; L
100.0%; Pred. No. 4.6e-112;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/026,320A
FILING DATE: 26-FEB-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609803
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPRECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Oldenkamp, David J
REGISTRATION NUMBER: 29421
REFERENCE/DOCKET NUMBER: 94
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3107885046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 3102771297
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 432 base pairs
TYPE: nucleic acid
                                               Matches 411; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Los Angeles
California
                           Similarity
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STRANDEDNESS:
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      Query Match
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APPLICANT: Ostberg, Lars G.

TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                         TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
                                                                                                                                           181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGGGGATCCCACATGG 240
                                                                                                                                                                                                                                                                                                TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
                                                                                                                                                                                                                                 361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-UN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-WAY-1988
PRIOR APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986
ATTORNEY,AGENT INFORMATION:
NAME: SMITH, WILLIAM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-UN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
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ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve.
CURRENY APPLICATION NATA:
APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08468671 Patent No. 5648077 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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:
Patent No. 5565354
GENERAL INFORMATION
APPLICANT: OStberg, Lars G.
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTTTTTGAAAGGTGTCCAGTGTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                             NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 252.2; DB 1
Pred. No. 2.6e-65;
0; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION NUMBER: US 06/925,196
FILING DATE: 10-OCT-1986
PRIOR APPLICATION NUMBER: US 06/925,196
FILING DATE: US 05/925,196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11823-50-7
                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-JUN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 393 BASE PAIRS
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.4%;
81.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 61.4
Best Local Similarity 81.5
Matches 335; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE: Hybridoma CELL LINE: ZM1-1
                                                                                                                                                                                                                                                                    ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                      USA
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; LOCATION:
US-08-259-372A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                            STATE:
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MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,372A
FILING DATE: 14-JUN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION NUMBER: US 06/925,196
FILING DATE: 11-MAY-1988
PRIOR APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION NUMBER: US 06/904,517
FILING DATE: US-SEP-1986
ATPONEY/AGENT INFORMATION:
NUMBER: US-SEP-1986
ATPONEY/AGENT INFORMATION:
NUMBER: US-SEP-1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Smith, william M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: PE1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 82.3
Matches 292; Conservative
        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..423
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US-08-259-372A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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Batent No. 556534

GENERAL INFORMATION:

APPLICANT: Ostberg, Lars G.

TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

GITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCCACATGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 TITCITCAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGICIAITACIGIGCGAGCIIG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 TATGCAGACTCCGTGAAGGCCCGATTCACCATCTCCAGAGAAATGCCAAGAACTCCTTG 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 252.2; DB 1; Length 393;
Pred. No. 2.6e-65;
0; Mismatches 58; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                        11823-50-7
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 1182:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
INFORMATION FOR SEO ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 61.4%;
Best Local Similarity 81.5%;
Matches 335; Conservative
                                                                                                                                      LENGTH: 393 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
CELL LINE: ZMI-1
                                                                                                                                                                                           MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTT-CENT
                                                                                                                                                                                                                                                                                                                                                                            ) NAME/KEY: CDS
; LOCATION: 1..393
US-08-468-671-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
                                                                                                                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-259-372A-1
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STATE:
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GTGCAGCTGGTGGAGTCTGGGGGGCGCTTGGCAAAGCCTGGGGGGTCCCTGAGACTCTGG 120
                                                                                                                                    | TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
                                                                                                                                                                                        Gaps
                                                                  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG 60
                                                                                                                                                                                                                              GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG
                                        9
            Length 423;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Freeman, John W. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                617-542-8906
    PE1-1
                                                                                                                                     Query Match
Best Local Similarity
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CITY: Boston
STATE: MA
  CELL LINE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                      ; NAME/KEY:
; LOCATION:
US-08-468-671-1
                                                                                                                                                                            Matches 292;
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ostberg, Lars G.
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
295 TITCTGCAAATGCACAGCCTGAGAGCTGCGGACACGGGTGTATATTACTGTGCGA 349
                                                                           301 TITCTICAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGTCIATIACIGIGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,671
                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Townsend and Townsend and Crew LL STREET: Two Embarcadero Center, Eighth Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION NUMBER: US 06/94,517
FILING DATE: 05-SEP-1986
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                              Sequence 1, Application US/08468671
Patent No. 5648077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30,223
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 423 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Smith, William M. REGISTRATION NUMBER: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
CELL TYPE: Hybridoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE
ORGANISM: HOR
                                                                                                                                                                                                                                                                                                                                                                                                                               S
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STATE:
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61 GTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCTGGGGAGGTCCCTGAGACTCTCC 120
                                                                                                                                                                                                           61 GTGCAGCTGGTGGAGTCTGGGGGCGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120
                                                                                                                                                                                                                                                                                                             121 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                  1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCGTTGCTCTTTTAAGAGGTGTCCAGTGTCAG 60
                                                                                                        1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Honjo, Tasuku
APPLICANT: Matsuda, Fumihiko
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 TITCTGCAAATGCACAGCCTGAGAGCTGCGGACACGGGTGTATATTACTGTGCGGA 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITCTICAAAIGAACAGCCIGAGAGGIGAGGACACGGCTGICIAITACTGTGCGA 355
                                                        9
     Length 423;
                                                        Indels
58.8%; Score 241.8; DB 1; ilarity 82.3%; Pred. No. 3e-62; Conservative 0; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSED for Windows Version 2.0
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION UNDER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06501/004001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Fish & Richardson, P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/08545809A Patent No. 6096878 GENERAL INFORMATION:
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ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            330 GGACACGGCTGTCTATTACTGTGCGAG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               600 GGACACGCCTGTATTACTGTGCGAG 626
                                                                                                                                                                                                                   ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                       Query Match 57.5%;
Best Local Similarity 85.0%;
Matches 278; Conservative
                                                 TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS: LENGTH: 743 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-545-809A-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 ACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAAGGGCAGATTCAC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCTCCAGAGAGACGCCAACAACACACTGTTTCTTCAAATGAACAGCCTGAGAGCTGA 329
                                                                                                                                                                                                                                                                                                                                                       90 GGCAAAGCCTGGGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTT 149
                                                                                                                                                                                                                                                                                                                                                                          150 CAATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                           315 ATCCATTAGTAGTAGTAGTACATACATACGAGACTCAGTGAAGGGCCGATTCAC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: HONJO, TASUKU
APPLICANT: HONJO, FUMINIKO
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE
NUMBER OF SEGURENCES: 145
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        .
9
                                                                                                                                                                                                                       Length 519;
                                                                                                                                                                                                                                                      43; Indels
                                                                                                                                                                                                                   Score 236.2; DB 3;
Pred. No. 1.5e-60;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette
COMPUTER: IDSK Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson, P.C. STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 GGACACGGCTGTCTATTACTGTGCGAG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-545-809A-48
; Sequence 48, Application US/08545809A
; Patent No. 6096878
                                                                                                                                   human İymphoblast
CGM1
                                                                                                                                                                                                                   57.5%;
85.0%;
               LENGTH: 519 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
                                                                                    Genomic DNA
                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.0°
Matches 278; Conservative
                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM CCC
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Freeman, John W.
REGISTRATION NUMBER: 2
                                                                                                                                 ; CELL TYPE:
; CELL LINE:
US-08-545-809A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: BOS
STATE: M.
COUNTRY:
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90 GCCAAAGCCTGGGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTT 149
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                                                                                                                                                                                                                                                                                                                                                                                        420 CAGTAGCTATAGCATGAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTTC 479
                                                                                                                                                                                                                                                                                                                                                                                                                                              210 ACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAAGGGCAGATTCAC 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                Sequence 11, Application US/08545809A
Patent No. 6096878
GENERAL INPORMATION:
APPLICANT: HONJO, Tasuku
APPLICANT: HONJO, Tasuku
APPLICANT: HONJO, Tasuku
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145
CORRESPONDENCE ADDRESS:
                                                                                                                                            150 CAATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  480 ATACATTAGTAGTAGTAGTAGTACCATATACTACGCAGACTCTGTGAAGGGCCGATTCAC
                                                         9
        Length 743;
                                                         Indels
                                                         43;
        DB 3;
Score 236.2; DB 3
Pred. No. 1.7e-60;
0; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: Windows95
SOFTWARE: Fast-E50 for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
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TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAACGCCCAACAACACACTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGA---- 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 TACCTGCAAATGAACAGTCTGAGGCTGAGGACACGGCCGTGTATTACTGTGCAAGGGAG 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     356 -----GCTTGACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTC 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 GACTACGGTATCCGGCCTGGTTTGCTTACTGGGGCCCAAGGGACTCTGGTCACTGTCTC 413
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Sequence 23, Application US/O8545809A

Patent No. 6096878

GENERAL INFORMATION:
APPLICANT: Honjo, Tasuku

APPLICANT: MATEUda, Fumihiko

TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
NUMBER OF SEQUENCES: 145

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 417;
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                                                                                          Version #1.30
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Pred. No. 2.6e-59;
0; Mismatches 82;
UISKETTE-3.50 inch, 1
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,346A
FILING DATE: 08-CT-1993
CLASSIFICATION:
ATTORNEY/AGENT
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Onofrio, Dara 1.
REGISTRATION NUMBER: 34,889
REFERENCE/DOCKET NUMBER: CLT 149,608
TELECOMMUICATION INFORMATION:
TELEPHONE: 212-826-6565
TELEFAX: 212-826-5909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: Fish & Richardson, P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.4%;
ilarity 76.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 417 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 319; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
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STREET: 22
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US-08-545-809A-23
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Sequence 49, Application US/08134346A

Sequence 49, Application US/08134346A

Patent No. 62813A-10N

GENERAL INFORMATION:

APPLICANT: do Couto, F.J.R.

APPLICANT: Cerlani, R.L.C.

APPLICANT: Petersen, J.A.

TITLE OF INVENTION: HYBRIDOMA AND ANTI-KC-4 HUMANIZED

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS

TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89 TGGCAAAGCCTGGGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCT 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209 CACGTATTAGTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAAGGGCAGATTCA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 TCAATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGGCAGGGGCTGGAGTGGGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269 CCATCTCCAGAGAGAACGCCAACACACACTGTTTCTTCAAATGAACAGCCTGAGAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 57.3%; Score 235.6; DB 3
Best Local Similarity 84.8%; Pred. No. 2.5e-60;
Matches 278; Conservative 0; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrager, Chong & Flaherty
STREET: 300 Park Avenue
                                                                                                                                    06501/004001
                    APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    625 AGGACACGCCGTGTATTACTGTGCGAG 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 AGGACACGGCTGTCTATTACTGTGCGAG 356
                                                                                      NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFRENCE/DOCKET NUMBER: 0650:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-6970
TELEFAX: 617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
CELL TYPE: human lymphoblast
CELL LINE: CGM1
                                                                                                                                                                                                 TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 715 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Genomic DNA ORIGINAL SOURCE:
  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-545-809A-11
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COUNTRY:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96 GCCTGGGGGGTCCCTGAGACTCTGGTGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1008 GCCTGGGGGGTCCCTGAGACTCTCTGTGCAGCCTCTG-----GATTCACCTTTAGCAG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 TAGTAGTAGTGGTGATCCCACATGGTACGCAGACTCCGTGAAGGGCAGATTCACCATCTC 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           276 CAGAGAGAACGCCAACAACACACTGTTTCTTCAAATGAACAGCCTGAGAGCTGAGGACAC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/08619491
Patent No. 6210670
GENERAL INFORMATION:
APPLICANT: Berg, Ellen L.
TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
TITLE, OF INVENTION: Specific for E-Selectin and P-Selectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 227.6; DB 3
Pred. No. 4.9e-58;
0; Mismatches 44
                                                                                  SYSTEM: Windows95
FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                          NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEPAX: 617-542-8906
                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER:
ELING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
APPLING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           GELL TYPE: human lymphoblast:
CELL TYPE: human lymphoblast:
GELL LINE: CGM1
US-08-545-809A-23
                                                                                                                                                                                                                                                                               TELEFAX: 61, TELEFAX: 61, TELEFAX: 61, TELEFX: 200154
INFORMATION FOR SEQ ID NO: 23: SEQUENCE CHARACTERISTICS: LENGTH: 514 base pairs "vp8: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 GGCTGTCTATTACTGTGCGA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 GGCCGTATATTACTGTGCGA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.4%;
Best Local Similarity 84.4%;
Matches 270; Conservative (
                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: Genomic DNA
                                                     Diskette
                                     COMPUTER READABLE FORM MEDIUM TYPE: Diskett
                                                                    COMPUTER: IBM COM
OPERATING SYSTEM:
SOFTWARE: FASTSEQ
                      02110-2804
         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-619-491-7
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181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAGAACGCCAACAACACACTG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 TITCTICAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGICIAITACIGIGCGAGCIIG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATGGAGTITGGGCTGAGCTGGTTTTCCTTGTTCCTTTTGAAAGGTGTCCAGTGTGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,491
FILING DATE: 26-MAR.1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 225.8; DB 4;
Pred. No. 1.5e-57;
0; Mismatches 102;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLI
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Storella, John R.
REGISTRATION NUMBER: 32,944
REFERENCE-DOCKET NUMBER: 011823-005810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUBER: WO PCT/US95/07302
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUBER: US 08/259,963

FILING DATE: 14-JUN-1994

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 54.9%;
Best Local Similarity 73.7%;
Matches 303; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                         ZIP: 94111-3834
COMPUTER READABLE FORM:
                                                                CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION:
; OTHER INFORMATION:
;
US-08-619-491-7
                                                                                    California
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MOLECULE TYPE: DNA
FEATURE:
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301 TITCITCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAGCTTG 360
                                                                                                          295 TATCTGCAAATGAACAGTCTAAGGGCTGAGGACACGGCCGTGTATTACTGTGCAAGACCT 354
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                                                                                                                                                                          355 TTACCCCCGTTTGCTTACTGGGGCCAAGGGACTTTGGTCACTGTCTCTGCA 405
                                                                                                                                                    361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCTCA 411
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HARFELDT, Elisabeth
APPLICANT: LAKE, Philip
APPLICANT: NOTTAGE, Barbara
APPLICANT: OSTBERG, LASS G.
TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERDES SIMPLEX
TITLE OF INVENTION: VIRUS AND CELL LINE PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "HSV863 heavy chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/305,683A
FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54.8%; Score 225.2; DB 1; 79.2%; Pred. No. 2.3e-57; ive 0; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 11823-005230
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 0S 07/759,279
FILING DATE: 13-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08305683A Patent No. 5646041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 326-2410
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 base pairs
TYPE: nucleic acid
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Best Local Similarity 79.2
Matches 282; Conservative
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                               RESULT 14
US-08-305-683A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAACGCCAACAACACACTG 300
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361 ACTACAGGGTCTGACTCCTGGGGCCAGGGAGTCCTGGTCACCGTCTCCTCA 411
                      355 TTACCCCGTTTGCTTACTGGGGCCAAGGGACTTTGGTCACTGTCTCTGCA 405
                                                                                                                                                                                      APPLICATE BEGG THEN L.
TITLE OF INVENTION: Cross-Reacting Monoclonal Antibodies
TITLE OF INVENTION: Specific for E-Selectin and P-Selectin
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 225.8; DB 5;
Pred. No. 1.5e-57;
0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11823-005810PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US95/07302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/259,963
FILING DATE: 14-JUNE-94
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,23
REFERENCE/DOCKET NUMBER: 11823-0(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
                                                                                                                     Tr.0595-07302-7
Sequence 7, Application PC/TUS9507302
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 54.9%;
Best Local Similarity 73.7%;
Matches 303; Conservative (
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..405
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PCT-US95-07302-7
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181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGGGGATCCCCACATGG 240
                                                                         TGCGCAGCCTCCGGGTTCAGGTTCACCTTCAATAACTACTACATGGACTGGGTCCGCCAG 180
                                                                                           241 TACGCAGACTCCGTGAAGGGCAGATTCACCATCTCCAGAGAAGGCCCAACAACACACTG 300
                                                                                                                                                                                                                                        295 TATCTGCAAATGAACAGCCTGAGAGCCGAGGACGACGCTGTGTATTACTGTGCGAA 350
                                                                                                                                                                                                                                                                                           301 TITCITCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTGTGCGAG 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hillman, Jennifer L.
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: We, Young, Janice
APPLICANT: We, Well C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
CORRESPONDENCE: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/09049672A Patent No. 6135941 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Pharmacs 1174 Porter Drive CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1572 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMARNOT03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIBRARY: BMARN
CLONE: 1669829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-09-049-672A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-049-672A-18
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240
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                                                                  9
                                                                                                                                                                             1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTTCCTCTTTTGAAAGGTGTCCAGTGTGAG
                                                                                                         61 GTGCAGCTGGTGGAGTCTGGGGGGGGCTTGGCAAAGCCTGGGGGGGTCCCTGAGACTCTGG
                                                                                                                                                                                                                  181 GCTCCAGGGCAGGGGCTGGAGTGGGTCTCACGTATTAGTAGTAGTGGTGATCCCACATGG
                                                                                                                                                                                                                                                                                                                             301 TITCTICAAAIGAACAGCCIGAGAGCIGAGGACACGGCIGICIAITACIGIGCGA 355
                                                                                                                                                                                                                                                                                                                                            ;
9
 Length 1572;
                           Indels
Score 224.2; DB 3;
Pred. No. 7.6e-57;
0; Mismatches 68;
Query Match 54.5%;
Best Local Similarity 79.2%;
Matches 281; Conservative
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Search completed: September 23, 2002, 18:00:56 Job time: 3227 sec

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                                                                                                                         ; Search time 6364.12 Seconds (without alignments).
1325.809 Million cell updates/sec
                                                                                                                                                                                                                                                            1 ATGGCCTGGACTCTGCTCCT......CCCGGTTGACCGTCCTAGGT 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/1/pna/US082_COMB.seq:*
/cgn2_6/ptodata/1/pna/US082_COMB.seq:*
/cgn2_6/ptodata/1/pna/US083_COMB.seq:*
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ptodata/1/pna/US096A_COMB.seq:*
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'ptodata/1/pna/US098A_COMB.seq:*
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ptodata/1/pna/US099A_COMB.seq:*
ptodata/1/pna/US099B_COMB.seq:*
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/cgn2_6/ptodata/1/pna/US081_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                       21979536 seqs, 10817449327 residues
                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                              September 23, 2002, 17:50:25
                                                                                  OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Maximum Match 100
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Sequence:

Title:

Run on:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ID	-09-019-44	-09-292-053	-09-878-1	-10-033-356-26	-09-396-88	US-09-396-885A-4438	9	9	9	9	9	9	-0	US-09-909-627-16098	US-09-235-076-16692	US-09-289-768-1488	ç	-09-737-223-16	-08-636-36	US-09-652-127-62	09-359-067	09-665-486-56		PCT-US02-04175-8	10-076-747-	-09-359-067-381	-489-036	-09-943-143-848	-665-486	-60-168-599	US-09-049-672-23
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RESOLT:

Sequence 1, Application US/09292053

Sequence 1, Application US/09292053

GENERAL INFORMATION:
APPLICANT: REFF. MITCHELL E.
APPLICANT: NAKAWURA, TAKEHIKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL ANTIBODIES AND USE
TITLE OF INVENTION: THEREOF AS THERABUTICS
FILE REFERENCE: 23522.0699

CURRENT APPLICATION NUMBER: US/09/292,053

CURRENT FILLING DATE: 1999-04-14

CURRENT FILLING DATE: 1999-04-14

CURRENT APPLICATION NUMBER: 08/803,085
                                                                                                                                                                                                                                                           240
                                                                                                                            61 TCTGCCCCGGACTCACCCTCCTCTGTGTCTGGGTCTCCTGGACACACGCGGTCACCATCTCC 120
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                         Gaps
                                                                                                             TCTGCCCCGACTCAGCCTCCTCTGTGTCTGGGTCTCCTGGACAGTCGGTCACCATCTCC 120
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                                                                                                                                                                                    GCTGAGGACGAGGCTGATTATTACTGTTGTTCATATACAACCAGTAGCACTTTGTTATTC 360
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100.0%; Pred. No. 3.8e-101;
ive 0; Mismatches 0;
            Pred. No. 3.8e-101;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                      361 GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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100.08; Fig.
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Best Local Similarity 100.
Matches 390; Conservative
          Best Local Similarity 100.
Matches 390; Conservative
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LOCATION: (1)..(58)
NAME/KEY: mat_peptide
LOCATION: (58)...(390)
NAME/KEY: CDS
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SOFTWARE: Patentin Ve
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LENGTH: 390
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US-09-292-053-1
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          20660, A
7751, Ap
21556, A
21556, A
7751, Ap
70521, A
70521, A
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KLOETZER, William S.
NAKAMURA, TAKEHIKO
TITLE OF INVENTION: GAMMA-1 ANTI-HUMAN CD23 MONOCLONAL
ANTIBODIES AND USE THEREOF AS THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,441
FILING DATE: OS-Feb-1998
CLASSIFICATION: CUNKnown>
PRIOR APPLICATION NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, LLP
STREET: P.O. BOX 1404
                     US-09-240-371-7751
US-09-277-27556
US-09-90-277-21556
US-09-919-724-7751
US-09-913-524-70521
US-09-933-524-70521
US-09-933-524A-70521
US-09-652-127-100
US-09-652-127-100
                                                                                                                                                                     US-60-168-599-73
US-09-699-999-2971
                                                                                                                                                                                                  US-09-489-036-8563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: TESKID, ROBIN L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-502
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/803,085
FILING DATE: 20-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                           ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-019-441-1
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09019441 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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58..390
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SEQUENCE CHARACTERISTICS
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          NAME/KEY:
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NAME/KEY: misc_feature
LOCATION: 549, 594
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Best Local Similarity
Matches 355; Conserv
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US-10-033-356-264
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APPLICANT: King, Gordon E.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF COLON CANCER;
FILE REPERBENCE: 210121.532
CURRENT APPLICATION NUMBER: US/09/878,134
CURRENT FILING DATE: 2001-06-07
NUMBER OF SEO ID NOS: 377
SOFTWARE: COTIXA INVENTION DISCLOSURE DATAbase
SEQ ID NO 264
LENGTH: 605
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Best Local Similarity 91.0%; Pred. No. 5e-85;
Matches 355; Conservative 0; Mismatches 35;
                                                                                                                                                                                                                                             GGAAGAGGGACCCGGTTGACCGTCCTAGGT 390
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US-09-878-134-264
; Sequence 264, Application US/09878134
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C
US-09-878-134-264
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APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE 1
TITLE OF INVENTION: AND DIRANOSIS OF COLON CANCER
FILE REFERENCE: 210121:532C1
CURRENT APPLICATION NUMBER: US/10/033,356
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred. No. 5e-85;
0; Mismatches 35;
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US-09-396-885-4438
Sequence 4438, Application US/09396885
GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Busfield. Samanths I
                                                              GGAAGAGGGACCCGGTTGACCGTCCTAGGT
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OTHER INFORMATION: n = A,T,C or G
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84.8%; Score 330.8; DB 17; Length 607;

Best Local Similarity 90.5%; Pred. No. 4.1e-84;

Matches 353; Conservative 0; Mismatches 37; Indels 0;
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-768
CURRENT APLICATION NUMBER: US/09/287,618
CURRENT APLICATION NUMBER: US/09/287,618
CURRENT FILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 35865
SOFTWARE: FactSEQ for Windows Version 3.0
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Pred. No. 1.4e-83;
0; Mismatches 37
                          NUMBER OF SEQ ID NOS: 5360
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4438
LENGTH: 607
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          1999-03-30
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90.5%;
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LOCATION: (1)...(607)
COTHER INFORMATION: n = A,T,C or
US-09-396-885A-4438
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Best Local Similarity
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US-09-287-618-20661
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LENGTH: 419
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GENERAL INFORMATION:
APPLICANT: Gearing, David P.
APPLICANT: Gearing, David P.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: HUMAN ESOPHAGUS LIBRARY
FILE REFERENCE: MAN98 48pM
CURRENT APPLICATION NUMBER: US/09/396,885A
CURRENT FILING DATE: 1999-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-09-15
PRIOR FILING DATE: 1998-10-30
PRÎOR APPLICATION NUMBER: 60/126,444
TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM A TITLE OF INVENTION: HUMAN ESOPHAGUS LIBRARY FILE REFERENCE: MLN98-48pm (CURRENT APPLICATION NUMBER: US/09/396,885); CURRENT FILING DATE: 1990-09-15; PRIOR APPLICATION NUMBER: 60/100,459 PRIOR FILING DATE: 1998-09-15; PRIOR FILING DATE: 1998-09-15; PRIOR FILING DATE: 1998-10-30; PRIOR FILING DATE: 1999-03-30; PRIOR FILING DATE: 1999-03-30; NUMBER OF SEQ ID NOS: 5360 (SOFTWARE: FastSEQ for Windows Version 3.0); SEQ ID NO 4438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 330.8; DB 1
Pred. No. 4.1e-84;
0; Mismatches 37
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90.5%;
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; OTHER INFORMATION: n = A,T,C (US-09-396-885-4438
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Matches 353; Conservative
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ORGANISM: Homo saptens
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
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US-09-396-885A-4438
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Roseberry, Ann M.
Wright, Rachel J.
Chen, Wensheng
Liu, Tommy
Yap, Pierre E.
Stockdreher, Theresa K.
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Greenawalt, Lila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amshey, Stefan
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CURRENT FILIR OPTER: 1999-12-01
SUGHRENT FILIR PROFILEM
SOFTHAMER: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 255510.168
US-60-168-599-592
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Matches 351; Conservative
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ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILE REFRERENCE: 20411-747CON1
CURRENT APPLICATION NUMBER: US/09/359,067
CURRENT FILING DATE: 1999-07-22
EARLIER APPLICATION NUMBER: US 09/131,598
EARLIER FILING DATE: 1998-08-10
NUMBER OF SEQ ID NOS: 44976
SOFTWARE: FastSEQ for Windows Version 3.0
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; OTHER INFORMATION: n = A,T,C
US-09-359-067-41768
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/332,782A
CURRENT FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASLSEQ for Windows Version 3.0
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89.5%; Pred. No. 2.5e-82;
iive 0; Mismatches 41;
                Score 324.4; DB 1
Pred. No. 2.5e-82;
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Matches 349; Conservative
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; ORGANISM: Homo sapiens
US-09-332-782-36573
                                Similarity
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                                   Best Local Sim
Matches 349;
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                                                                                                            APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/235,076
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES.
FILE REFERENCE: 20411-766
CURRENT APPLICATION NUMBER: US/09/277,227
CURRENT FILING DATE: 1999-03-25
NUMBER OF SEQ ID NOS: 23680
SOFTWARE: FASTSEQ for Windows Version 3.0
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Pred. No. 2.5
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415 ttcggcggaggaccaagctgaccgtcctaggt
                                                                             Sequence 36573, Application US/09235076 GENERAL INFORMATION:
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Best Local Similarity 89.5%;
Matches 349; Conservative
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US-09-235-076-36573
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US-09-277-227-16098
                                                                US-09-235-076-36573
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LENGTH: 408
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                                                                                                                                                                                           Sequence 36573, Application US/09737233
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TILLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/737, 223
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 09/332,782
PRIOR FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16098, Application US/09909627
GENERAL INFORMATION
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 324.4; DB 2
Pred. No. 2.5e-82;
0; Mismatches 41
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 36573
LENGTH: 408
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CORGANISM: Homo sapiens
US-09-737-223-36573
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Best Local Similarity
Matches 349; Conserv
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US-09-737-223-36573
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GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/235,076
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                 DB 34;
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Pred. No. 2.5e-82;
); Mismatches 41.
                                                                                                                                                                                                                                                                                                                                            Score 324.4; DB 3
Pred. No. 2.5e-82;
0; Mismatches 41
ON: FROM VARIOUS CDNA LIBRARIES 20411-766
      TITLE OF INVENTION: FROM VARIOUS CDNA LIBRAR, FILE REFERENCE: 2041-766
CURRENT APPLICATION NUMBER: US/09/909,627
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/277,227
PRIOR FILING DATE: 1999-03-23
NUMBER OF SEQ ID NOS: 23680
SOFTWARE: FASESEQ for Windows Version 3.0
SEQ ID NO 16098
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Best Local Similarity 89.5%;
Matches 349; Conservative 0
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Matches 349; Conservative
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US-09-909-627-16098
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Best Local Similarity
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US-09-235-076-16692
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